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GenCore version 5.1.6
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OM protein - protein search, using sw model

8, 2005, 16:04:41; Search time 39 Seconds (without alignments) 350.328 Million cell updates/sec Run on:

US-10-723-083-2 Title:

Perfect score:

765 1 MHHHHHHSSGIEGRMAPARS.......ENLKDFLLVIPFDCWEPVQE 142 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
3: pir2:*
: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de				
Result No.	Score	Query	Query Match Length	DB	ID	Description
	673	88.0	144	-	FOHUGM	granulocyte-macrop
7	548	71.6	144	7	JH0469	granulocyte-macrop
m	544	71.1	144	٦	A61632	granulocyte-macrop
4	480.5	62.8	143	ч	FQBOGM	granulocyte-macrop
	473	61.8	144	~	A44936	granulocyte-macrop
9	441	57.6	127	~	146269	granulocyte-macrop
7	367.5	48.0	153	٦	FOMSGM	granulocyte-macrop
œ	84.5	11.0	2493	7	S72349	nonstructural poly
σ	81	10.6	305	~	A56554	transcription fact
10	81	10.6	359	~	A55839	transcription fact
11	80.5	10.5	285	~	AH2390	tetrapyrrole methy
12	80.5	10.5	2493		S26372	nonstructural poly
13	79	10.3	610		A57632	homeotic protein E
14	78.5	10.3	329		T45972	hypothetical prote
15	78	10.2	496		S25091	cruciferin BnC2 -
16	78	10.2	816		S05548	
17	78	10.2	1019		T00117	dve protein - frui
18	77.5	10.1	420		T39712	hypothetical prote
19	77.5	10.1	427	N	T42516	
20	75.5	9.9	292	~	151171	transcription fact
21	75.5	9.6	942	~	JC2129	protein kinase PKN
22	75.5	9.9	1016	~	A46079	protein kinase C (
23	75	9.8	605	-	QQBE29	BRLF1 protein - hu
24	74.5	9.7	384	7	T41302	ferrochelatase pre
25	74.5	9.7	1305	~	T18548	flax rust resistar
56	73.5	9.6	248	~	T02647	probable MADS-box
27	73.5	9.6	1622	~	JE0378	DNA (cytosine-5-)-
28	73	9.5	234	~	T26429	2
29	73	9.5	461	7	S34472	MFH-1 protein - mc

PSD-95/SAP90-assoc protein F25G6.2 [i	probable retroelem hypothetical prote Frz CD protein – M	probable mitochond tryptophan 5-monoo RNA-directed RNA p	DNA helicase - Aqu hypothetical prote transforming prote	glutamine-fructose proline-rich prote transcription fact	serine/threonine-s exodeoxyribonuclea
T03306 A89135	T00499 D83709 C32185	G86383 A34582 PN0105	D70476 T00338 TVFVVR	F82951 T46089 B56564	A26030 H81751
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943 1183	1496 289 417	311 447 770	530 1273 398	611 265 601	633 1025
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73	73 72.5 72.5	72 72 72	71.5 71.5 71	70.5	70.5
30	33 33 4	35 37	3.9 3.9 4.0	4 4 4 1 2 6	4 4 5

ALIGNMENTS

RESULT 1
FQHUGM
granulocyte-macrophage colony-stimulating factor precursor [validated] - human
N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004
C;Accession: C24636; IS9065; A25169; A01853; A44175; JC1090
R; Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
EMBO J. 4, 2561-2568, 1985
A; Title: Structure of the chromosomal gene for granulocyte-macrophage colony stim
A;Reference number: A91015; MUID:86030234; PMID:3876930
A;Accession: C24636
A; Molecule type: DNA
A;Residues: 1-144 <miy></miy>
A;Cross-references: UNIPROT:P04141; EMBL:X03021; NID:g31858; PIDN:CAA26822.1; PID
R; Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Adamson, J
Proc. Natl. Acad. Sci. U.S.A. 83, 3101-3105, 1986
A; Title: Genomic cloning, characterization, and multilineage growth-promoting act
A; Reference number: I59065; MUID:86205844; PMID:3486413

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(D:g31859 J.W. tivity of

A;Accession: 159065
A;Status: translated from GB/EWBL/DDBJ
A;Restus: translated from GB/EWBL/DDBJ
A;Residues: 1-144 <RES>
A;Cross-references: GB:M13207; NID:g181147; PIDN:AAA98768.1; PID:g181148
A;Cross-references: GB:M13207; NID:g181147; PIDN:AAA98768.1; PID:g181148
B;Cantrall, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R., Proc. Natl. Acad. Sci. U.S.A. 82, 6250-6254, 1985
A;Title: Cloning, sequence, and expression of a human granulocyte/macrophage colony-stimmal, R;Reterence number: A25169; MUID:85298329; PMID:3898082
A;Rolecule type: mRNA
A;Residues: 1-144 <CAN>
A;Residues: 1-144 <CAN>
A;Residues: 1-144 <CAN>
A;Cross-references: GB:M11734; NID:g181149; PIDN:AAA52122.1; PID:g181150
R;Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.; Luh, J.; Arai, K.; Rennick, I Proc. Natl. Acad. Sci. U.S.A. 82, 4360-4354, 1985
A;Itle: Isolation of CDNA for a human granulocyte-macrophage colony-stimulating factor & A;Reference number: A01853; MUID:85242684; PMID:3925454

D.400 P Z ~ 20 E

A; Accession: A01873
A; Accession: A01875
A; Molecule type: mENA
A; Residues: 1-144 < LEE>
A; Cross-references: GB: M11220; NID: 9183363; PIDN: AAA52578.1; PID: 9183364
A; Cross-references: GB: M11220; NID: 9183363; PIDN: AAA52578.1; PID: 9183364
A; Cross-references: GB: M11220; NID: 9183363; PIDN: AAA52578.1; PID: 9183364
A; Clark, S.C.
Science 228, 810-815, 1985
A; Title: Human GM-CSF: molecular cloning of the complementary DNA and purification of the A; Reference number: A44175; MUID: 85218749; PMID: 3923623

A,Molecule type: mRNA A;Residues: 1-116, T',118-144 <WON> A;Cross-references: GB:M10663; ND:g181145; PIDN:AAA52121.1; PID:g181146 A;Across-references: G this sequence, including the amino end of the mature protein, were conf-R;Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y. Acta Biochim. Biophys. Sin. 25, 651-655, 1993

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Similarity 68.5
87; Conservative
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Best Local S:
Matches 87
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NyAlternate names: colony-stimulating factor 2; GM-CSF
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: JH0469; S16730
C;Accession: JH0469; S16730
R;McInnes, C.J.; Haig, D.M.
Gene 105, 275-279, 1991
A;Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-s
A;Reference number: JH0469; MUID:92039044; PMID:1937025
A;Accession: JH0469; MUID:92039044; PMID:1937025
A;Reference number: JH0469; MUID:92039044; PMID:1937025
A;Residues: 1-144 ACIA
A;Residues: 1-144 ACIA
A;Residues: 1-144 CMIPROT:P28773; GB:XS3561; NID:g18800; PIDN:CAA37632.1; PID:g18801
C;Comment: This protein is a glycoprotein cytchkine produced and secreted by various cell
C;Comment: This protein is a glycoprotein gravulating factor
C;Comment: This spratulocyte-macrophage colony-stimulating factor
C;Keywords: cytchkine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-17/Domain: signal sequence #status predicted &SIG>
F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status predicted
F;44/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                A, Accession: JC1090
A, Molecule type: protein
A, Residues: 18-21, 'C', 23-96, 'L', 98-144 < WEN>
A, Residues: 18-21, 'C', 23-96, 'L', 98-144 < WEN>
A, Residues: 18-21, 'C', 23-96, 'L', 98-144 < WEN>
A, Residues: 18-21, 'C', 23-96, 'L', 98-144 < WEN>
C, Genetics:
A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: 54, 31, 109/3
A, Introns: 53/3; 67/3; 109/3
B, Introns: 53/3; 109/3
B, In
Amplification of human granulocyte-macrophage colony-stimulating factor CDNA wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 673; DB 1; Length 144;
Pred. No. 2.8e-57;
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                                         A, Reference number: JC1090
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Matches 102; Conserv
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granulocyte-macrophage colony-stimulating factor precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: A61632
R;O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
Immunol. Cell Biol. 69, 51-55, 1991
A;Fitle: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stimm. A;Fitle: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stimm. A;Status: preliminary, not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-144 <OABs.
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CiAccession: Jul037
Rivaliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wignall, J.M.; Picha, K.S.; Cosman Mol. Immunol. 25, 843-850, 1988
A,Title: Bovine GM-CSF: molecular cloning and biological activity of the recombinant prot A,Reference number: Jul037; MUID:89096971; PMID:3062386
A,Rocassion: Jul037
A,Rocassion: Jul037
A,Rocassion: Jul037
A,Rocassion: Jul33 < MAL>
A,Rocassion: Jul33 < MAL>
C,Comment: This glycoprotein induces granulocyte, macrophage, and eosinophil colony forme C,Superfamily: granulocyte-macrophage colony-stimulating factor
C,Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F,1-17/Domain: signal sequence #status predicted < Signal Sequence #status pr
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C;Superfamily: granulocyte-macrophage colony-stimulating factor
F;1-17/Domain: signal sequence #status predicted <SIG>
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68.5%; Pred. No. 7.6e-39;
iive 20; Mismatches 19
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Accession: A24636
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granulocyte-macrophage colony-stimulating factor precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A44936
Blood 78, 930-937, 1991
A;Title: Molecular cloning and in vivo evaluation of canine granulocyte-macrophage colon
A;Reference number: A44936; MuID:91329842; PMID:1868252
A;Accession: A44936
A;Accession: preliminary
A;Molecule type: mRNA
A;Residues: 1-144 <NAS>
A;Coss-references: UNITROT:P48749; GB:S49738; NID:g233566; PIDN:AAB19466.1; PID:g233567
A;Note: sequence extracted from NCBI backbone (NCBIN:49739, NCBIP:49739)
C;Superfamily: granulocyte-macrophage colony-stimulating factor
F;1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulocyte-macrophage colony stimulating factor - rat (fragment)

G.Species: Rattus norvegicus (Norway rat)

G.Species: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004

G.Accession: 146269

R.Smith, L.R.; Lundeen, K.A.; Diveley, J.P.; Carlo, D.J.; Brostoff, S.W.

A.Title: Nucleotide sequence of the Lewis rat granulocyte-macrophage colony stimulating

A.Reference number: 146269; MUD: 94041474; PMID: 8225444

A.Accession: 146269

A.Accession: 146269

A.Moleoule type: mRNA

A.Moleoule type: mRNA

A.Mosedues: 1-17 < SMI>

A.Residues: 1-17 < SMI>

A.Residues: 1-17 < SMI>

A.Koss-references: UNIPROT: P48750; EMBL: UDDB: 322779; PIDN: AAA18281.1; PID: 93927

G.Superfamily: granulocyte-macrophage colony-stimulating factor
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68.5%; Pred. No. 4e-38;
:ive 19; Mismatches 2
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138 CWKPVKK 144
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CWKPVQK 127
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Matches 80; Conserv
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Best Local Similarity
Matches 87; Conserv
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: mRNA
A,Rolecule type: mRNA
A,Residues: 13-153 <RE2>
A,Cross-references: EMBL:X02333; NID:g51103; PIDN:CAA26193.1; PID:g51106
R,Myatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
EMBO J. 4, 2561-2568, 1985
A,Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating
A,Reference number: A91015; MUID:86030234; PMID:3876930
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A; Residues: 13-150, 'G', 152-153 <MIY>
A; Residues: 13-150, 'G', 152-153 <MIY>
A; Cross-references: GB:X03020; NID:g51099; PIDN:CAA26821.1; PID:g51099
A; Note: the sequence translated from the mRNA differs from that of the DNA in having 151-
R; Stanley, E.; Metcalf, D.; Sobieszczuk, P.; Gough, N.M.; Dunn, A.R.
BRBO J. 4, 2569-2573, 1985
A; Title: The structure and expression of the murine gene encoding granulocyte-macrophage
A; Reference number: A24645; MUID:86030235; PMID:3876931
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A; Residues: 13-153 < DEL>
A; Residues: 13-153 < DEL>
A; Cross-references: GB:X03019; NID:g51100; PIDN:CAA26820.1; PID:g736260
B; Gough, N.M.; Gough, J.; Metcalf, D.; Kelso, A.; Grail, D.; Nicola, N.A.; Burgess, A.W.,
Nature 309, 763-767, 1984
A; Title: Molecular cloning of cDNA encoding a murine haematopoietic growth regulator, gri
A; Reference number: A01854; WUID:84245825; PMID:6610831
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R;Sparrow, L.G.; Metcalf, D.; Hunkapiller, M.W.; Hood, L.E.; Burgess, A.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 292-296, 1985
A;Fitle: Purification and partial amino acid sequence of asialo murine granulocyte-macrog A;Reference number: A21882; MUID:85113187; PMID:3871523
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C;Superfamily: granulocyte-macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-29/Domain: signal sequence #status predicted <SIG>-
F;30-153/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA
F;95,104/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P01587; EMBL:X02333; NID:g51103; PIDN:CAA26192.1; PID:g51104
A;Accession: 148369
granulocyte-macrophage colony-stimulating factor precursor - mouse
NyAlternate names: colony-stimulating factor 2; GM-CSF; integral membrane protein
C;Species: Mus musculus (house mouse)
C;Daccess: Nus musculus (house mouse)
C;Accession: 148368; 148369; A24636; A24645; A24644; A01854; A21882
R;Gough, N.M.; Metcalf, D.; Gough, J.; Grail, D.; Dunn, A.R.
RyGough, N.M.; Metcalf, D.; Gough, J.; Grail, D.; Dunn, A.R.
A;Title: Structure and expression of the mRNA for murine granulocyte-macrophage colony
A;Reference number: 148368; MUID:85230331; PMID:3874057
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A;Residues: 13-150, 'G',152-153 <STA>
A;Cross-references: GB:X03020; NID:gS1098; PIDN:CAA26821.1; PID:g51099
R;DeLamarter, J.F.; Mermod, J.J.; Liang, C.M.; Eliason, J.F.; Thatcher,
EMBO J. 4, 2575-2581, 1985
A;Reference number: A24644; MUID:86030236; PMID:3902470
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A;Residues: 36,'1',38-150,'S',152-153 <GOU>
A;Cross-references: GB:X05906; NID:g51096; PIDN:CAA29336.1; PID:g51097
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A,Molecule type: protein
A,Residues: 36,′1',38-69 <SPA>
C,Comment: It is unclear if Met-1 or Met-13 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 48.0%; Score 367.5; DB 1; Best Local Similarity 54.3%; Pred. No. 5.5e-28; Matches 69; Conservative 23; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-153 <RES>
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001.
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q8YN88; GB:BA000019; PIDN:BAB76379.1; PID:g17133817; GSPDB:Gh
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a biphasic activation of NF-ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology F;206-238/Domain: ankyrin repeat homology <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tetrapyrrole methylase family protein [imported] - Nostoc sp. (strain PCC 7120) C; Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: AH2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ů,
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                                                                234 NK------PEPTCGRTPLHLAVEAQAASVLELLLKAGADPTARMYGGRTPLGSAL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 PSPSTOPWEHVNALQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL-ELYKQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                          46
                                                                                                                                                                                                                                                                                                                                                                                                                           Canastription factor inhibitor I-kappa-B-beta - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: ASS839
R;Thompson, J.E.; Phillips, R.J.; Erdjument-Bromage, H.; Tempst, P.; Ghosh, B.;Thompson, J.E.; Phillips, R.J.; Erdjument-Bromage, H.; Tempst, P.; Ghosh, A;Ttle: IkappaB-beta regulates the persistent response in a biphasic active A;Reference number: A55839; MUID:95171452; PMID:7867065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----HVNAIQEARRLINLSRDTAAEM
                                                                                                                                                                                                                     249 KAKARN--VETQQKVFELSSDNDKLRKRVEQLSRELETLRGIFRQLPESSLVKAMG 302
                                                                                                                                                                       -QEPTCLQTRLELYKQGLRGSLTKLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
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10.5%; Score 80.5; DB 2; Length 285;
Best Local Similarity 23.8%; Pred. No. 3.7;
Matches 29; Conservative 25; Mismatches 43; Indels 2
                              -TOPWEHVNAIQ-EARRLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 359;
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llarity 20.0%; Pred. No. 4.4;
Conservative 19; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 HHSSGIEGRMAPARSPSPSTQPWE-----
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A,Gene: all4680
C,Superfamily: methyltransferase, YraL type
                                  HHHHHH - - SSGIEGRMAPARSPSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 ----TMMASHYKQHCPPTPE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 LRPNPILARLLRAHGAPEPE 302
                                                                                                                                                                               47 TAAEMNETVEVISEMFDL---
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hes 28; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-359 <THO>
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A; Status: preliminary
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Matches
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A, Molecule type: mRNA
A, Molecule 1-305 «XIII»
A, Cross-references: UNIPROT: Q91346; GB: S44193; NID: 9255566; PIDN: AAB23276.1; PID: 9255567
A, Note: sequence extracted from NCBI backbone (NCBIN: 113707, NCBIP: 113708)
C, Superfamily: CCAAT/enhancer-binding protein alpha
C, Keywords: DNA binding; leucine zipper; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onstructural polyprotein - eastern equine encephalomyelitis virus
NyAlternate names: nonstructural protein NSP1; nonstructural protein NSP2; nonstructural Cispecies: eastern equine encephalomyelitis virus
Cispecies: eastern equine encephalomyelitis virus
Cispecies: eastern equine encephalomyelitis virus
CiAccession: 572349
RiWeaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.J.
Virology 197, 375-390, 1993
A;Title: A comparison of the nucleotide sequences of eastern and western equine encephal A;Reference number: S72349
A;R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q88789; EMBL:U01034; NID:9393006; PIDN:AAC53734.1; PID:93930 A;Orce: readthrough of the terminator UGA occurs between the codons AAU for residue 1878 A;Note: the readthrough stopcodon UGA for residue 1879 is translated as X C;Superfamily: Semliki Forest virus nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ISEMPDLOEPT---CLOTRLELY-KOGLRGSLTKLKGPLTMMASHYKOHC-PPTPETS--- 110
                                                                                                                                            76 LYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
                                                                                                                                                                                      30 APTRSPITUTRPWRHVEAIKEA---LNLLDDMPVTLNEEVEVVSNBFSFKKLTCVQTRLK 86
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NyAlternate names: CCAAT/enhancer core binding protein
C;Specides: Xenopus laevis (African clawed frog)
C;Date: 21-Uul-1995 #sequence_revision 21-Uul-1995 #text_change 09-Jul-2004
C;Accession: A5654
R;Xu, Q.; Tata, J.R.
R;Xu, Q.; Tata, J.R.
A;Title: Characterization and developmental expression of Xenopus C/EBP gene.
APARSPSPSTQPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Indels
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26.1%; Pred. No. 21;
ive 17; Mismatches
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                                                                                                                                                                                                                                                                                                     CWEPVQE 142
                                                                                                                                                                                                                                                                                                                                                                         147 CKKPVQK 153
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A;Cross-references: UNIPROT:Q38897; GB:U39944; NID:g1122532; PIDN:AAB05099.1; PID:g11225:
C;Genetics:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica napue
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C;Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: 825091
R;Breen, J.P.; Crouch, M.L.
R;Breen, J.P.; Crouch, M.L.
A;Title: Molecular analysis of a cruciferin storage protein gene family of EA;Reference number: $25090; MUID:92379259; PMID:1511129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                          2 HHHHHHSGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNE----TV
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                                                                    A,Gene: BEL1
C,Superfamily: unassigned homeobox proteins; homeobox homology
C,Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;391-450/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                     30;
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                                                                                                                                                                                                                                                            Length 610;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; MOJECCUE TYPE: DNA
A; Residues: 1-329 < DNA
A; Cross-references: UNIPROT: Q9M2K4; EMBL: AL137081
A; Experimental source: cultivar Columbia; BAC clone F9D24
                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%; Score 78.5; DB 2; 28.0%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                     Query Match
10.3%; Score 79; DB 2;
Best Local Similarity 22.7%; Pred. No. 13;
Matches 27; Conservative 20; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 95/1; 222/2; 362/3
C;Superfamily: glycinin
C;Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 AAGNNYNESDEVQSQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 DTAAEMNETVEVISE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S25091
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-496 <BRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3
A;Introns: 208/2; 238/3; 281/1
A;Note: F9D24.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T45972
A; Status: preliminary
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A; Residues: 1886-3493 <VO2>
A; Cross-references: EMBL:X63135; NID:959185; PIDN:CAA44847.1; PID:91334981
A; Cross-references: EMBL:X63135; NID:959185; PIDN:CAA44847.1; PID:91334981
A; Cross-references: EMBL:X63135; NID:959185; PIDN:CAA44847.1; PID:91334981
A; Note: this reading frame extends between two stop codons and does not begin with a sta C; Superfamily: Semilki Forest virus nonstructural protein
F;1-532/Product: nonstructural protein NSP1 #status predicted <NS3>
F;1327-1878/Product: nonstructural protein NSP2 #status predicted <NS3>
F;1886-2493/Product: nonstructural protein NSP3 #status predicted <NS3>
F;1886-2493/Product: nonstructural protein NSP4 #status predicted <NS3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonstructural polyprotein - eastern equine encephalomyelitis virus
N;Contains: nonstructural protein NSP1; nonstructural protein NSP2; nonstructural protein C;Species: eastern equine encephalomyelitis virus
C;Species: eastern equine encephalomyelitis virus
C;Accession: 226369; 256372
R;Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V.
Mol. Gen. Mikrobiol. Virusol. 5, 8-15, 1991
A;Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus genc
A;Reference number: S26369; MuID:91375524; PMID:1896061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: genomic RNA
A;Residues: 1-2493 <VOL>
A;Cross-references: UNIPROT:Q66581; EMBL:X63135
A;Otes: sequence could not be checked because of bad print in paper
A;Note: readthrough of the terminator UGA occurs between the codons AAU for residue 1878
A;Note: the readthrough stopcodon UGA for residue 1879 is translated as X
A;Accession: $26372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A57632
| Nomeotic protein BEL1 - Arabidopsis thaliana | C.Species Arabidopsis thaliana (mouse-ear cress) | C.Species Arabidopsis thaliana (mouse-ear cress) | C.Species Arabidopsis thaliana (mouse-ear cress) | C.Species A57632 | C.Species OS-Jul-2004 | C.Species OS-Jul-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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PAKGQQRREHLEALQTESRTL-IFYESPHRLRETLQDLAEVWGSDRQIVLARELTKLYEE 200
                                                                                                                          ---AIAHYQQKEPQGEYTLLVAGNPPSET----LLTEEQLKAELQQL 248
                                                                            ----PTPETSCATQIITFESFKENLKDF 128
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A;Residues: 1-610 <REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Indels
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1 Similarity 27.8%; Pred. No. 52;
37; Conservative 19; Mismatchee
                                                                    80 GLRGSLTKLKGPLTMMASHYKQHCP-
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1798 ITFDSVAEILEDF 1810
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                         201 FWRGSIGE
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MM 250
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Search completed: March 8, 2005, 16:14:10 Job time : 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 8, 2005, 15:56:25; Search time 177 Seconds (without alignments) 410.821 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-723-083-2 765 1 WHHHHHHSGIEGRMAPARS......BULKDFLLVIPFDGWEPVQE 142

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P04141 homo sapien		Q9g144 macaca mula	Q865y5 papio anubi	_	_	P51748 cervus elap	Q8wn17 equus cabal	Q95110 equus cabal		Q6q8a7 bubalus bub					P48750 rattus norv			_	Q99j91 marmota mon	P01587 mus musculu		Q6eny6 oryza sativ	Q8iyk2 homo sapien	Q8ndl5 homo sapien		-	-		-	Q8thk7 methanosarc
SUMMAKIES	ID	CSF2 HUMAN	Q647 <u>J</u> 8	Q9GL44	Q865Y5	CSF2 SHEEP	Q9MYK4	CSF2_CEREL	Q8WN17	Q95L10	CSF2_PIG	Q6Q8 <u>A</u> 7	CSF2 BOVIN	CSF2_CANFA	Q7YRF7	CSF2_FELCA	CSF2_RAT	CSF2 CAVPO	Q8VH40	Q8CFB5	099391	CSF2_MOUSE	Q80XG1	QGENY6	QBIYK2	QBNDL5	Q8N7T5	HUNB_DROAA	088789	Q647M8	QBMQP8	Q8THK7
	DB	7	~	~	7	-	7	-	7	~	-	~		-	7	н -	-	7	7	2	2	-	7	2	2	7	2	٠	2	~	7	~
	Length	144	144	144	144	144	144	144	146	152	144	143	143	144	141	144	127	140	14]	145	138	141	8	233	499	354	499	196	2493	424	785	606
d	ouery Match Length DB	88.0	8.98	85.4	82.7	71.6	71.1	69.0	68.8	67.1	63.7	63.6	62.8	61.8	61.7	59.0	57.6	56.9	55.2	49.9	47.2	47.1	27.4	11.4	11.4	11.1	11.1	11.0	11.0	10.8	10.8	10.8
	Score	673	664	653	633	548	544	528	527	513	487	486.5	480.5	473	472	451	441	435.5	422.5	381.5	361	360.5	209.5	87	87	82	æ	84.5	84.5	83	83	83
	Result No.	1	7	m	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

09cs72 mus musculu Q8ryl3 oryza sativ Q8jzs5 rattus norv Q8kt4 rattus norv Q46254 scaptomyza Q91346 xenopus lae Q60778 mus musculu Q8sb73 oryza sativ Q7g647 oryza sativ Q64e31 uncultured Q8xBMS anabaena sp	,,
09CS72 08RYL3 08RYL3 08LZS5 08K4T4 HUNB SCAAL 091346 09DG50 IKBB MOUSE 08VCZ7 05GST3 07GED7 064E31	Q / QRMIS
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610 3410 1212 1212 171 171 343 343 379 424 424 424	1761
100.00 100.00 100.00 100.00 100.00	10.5
82.5 81.5 81.5 81.5 81 81 81 81 81 81 81	90.0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 0

ALIGNMENTS

RESULT 1

CSF2	HUMAN
qi	CSF2 HUMAN STANDARD; PRT; 144 AA.
AC	NFI6;
DŢ	(Rel. 03, Creat
TO	03, Last
DŢ	
DE	Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE	(Colony-stimulating factor) (CSF) (Sargramostim) (Molgramostin).
NS S	Name=CSF2; Synonyms=GMCSF;
SO	ıs (Human).
ပ္ပ	
00	ia; Primates;
X O	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	INE=85242684; PubMed=3925454;
RA	Lee F., Yokota T., Otsuka T., Gemmell L., Larson N., Luh J.,
RA	Arai KI., Rennick D.;
RT	"Isolation of cDNA for a human granulocyte-macrophage colony-
RT	stimulating factor by functional expression in mammalian cells.";
RL	c. Natl.
RN	[2]
RP	SEQUENCE FROM N.A.
X	
RA	Kaushansky K., O'Hara P.J., Berkner K., Segal G.M., Hagen F.S.,
RA	Adamson J.W.;
RT	
RT	activity of human granulocyte-macrophage colony-stimulating factor.";
RL	
RN	
RP	SEOUENCE FROM N.A.
RX	MEDLINE=85298329; PubMed=3898082;
æ	Cantrell M.A., Anderson D., Cerretti D.P., Price V., McKereghan K.,
RA	Tushinski R.J., Mochizuki D.Y., Larsen A., Grabstein K., Cosman D.;
RT	"Cloning, sequence, and expression of a human granulocyte/macrophage
RT	colony-stimulating factor.";
RL	Proc. Natl. Acad. Sci. U.S.A. 82:6250-6254 (1985).
RN	[*
RP	SEOUENCE FROM N.A.
RX	
R.A	kens K.M.,
RA	E.L., Kay R.M., Orr E.C.
RA	C Golde D.W., Kaufman R.J., Hewick R.N
RA	
RT	"Human GM-CSF: molecular cloning of the complementary DNA and
RT	purification of the natural and recombinant proteins.";
RL	Science 228:810-815(1985).
RN	[5]
RP	SEQUENCE FROM N.A.
RX	
RA	Lee
RT	"Structure of the chromosomal gene for granulocyte-macrophage colony
RT	stimulating factor: comparison of the mouse and human genes.";

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A CATOLOGY OF EXCUSATION OF EXECUSATION OF EXECUSAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 LYKQGLRGSLTKLKGPLT#MASHYKQHCPPTPETSCATQIITFESFKBNLKDFLLVIPFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                              Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 APARSPSPSTQPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O-linked; partial.
N-linked (GlCNAC. .).
N-linked (GlCNAC. .).
T -> I (in dbSNP:2069640).
/FTId=VAR 013089.
I -> T (in dbSNP:25882).
/FTId=VAR 001975.
M -> K (in Ref. 8).
F -> L (in Ref. 8).
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Last sequence update)
Last annotation update)
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88.0%; Score 673; DB 1; I

Best Local Similarity 100.0%; Pred. No. 1.4e-54;

Matches 127; Conservative 0; Mismatches 0;
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Q647JB;
25-OCT-2004 (TEMBLrel. 28,
25-OCT-2004 (TEMBLrel. 28,
25-OCT-2004 (TEMBLrel. 28,
                      EMBL; AF510855; AAM44054.1;
PIR; C24636; FQHUGM.
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ID 0647,
AC 0647,
DT 25-0,
DT 25-0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARMACEUTICAL: Available under the names Leukine (Immunex) and Leucomax (Novartis). Used in myeloid reconstitution following bone marrow transplant engrathement failure or delay, mobilization and following transplantation of autologous peripheral blood progenitor cells, and following induction of eneotherapy in older adults with acute myelogenous leukemia. SIMILARITY: Belongs to the GM-CSF family.

DATABASE: NAME=Leukine; NOTE=Clinical information on Leukine;

WWW="http://www.leukine.com/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITES.

MEDLINE-29144669; PubMed=1737041;

MEDLINE-29144669; PubMed=1737041;

"Raushansky K., Lopez J.A., Brown C.B.;

"Role of carbohydrate modification in the production and secretion of human granulocyte macrophage colony-stimulating factor in genetically engineered and normal mesenchymal cells.";

Biochemistry 31:1881-1886(1992).
                    [6]
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SEQUENCE FROM N.A.
Cheng J., Connolly K.S., Gunning K.M.,
Davis C.A., Kadner K., Miguel T., Pitluck S., Pollard M., Rojeski H.,
Subramanian S., Martin C.H.,
Subramanian S., Martin C.H.,
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92235844; PubMed=1569568;
Walter M.R., Cook W.J., Ealick S.E., Nagabhushan T.L., Trotta P.P.,
Bugg C.E.;
                                                                                                                                                                                                                   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi
Nickerson D.A.;
ScattleSNPs. MHLBI HL66682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diederichs K., Boone T., Karplus P.A.; "Novel fold and putative receptor binding site of granulocyte-macrophage colony-stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Peripheral blood;
Bhattacharya P., Pandey G., Mukherjee K.J.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 18-144 FROM N.A., AND VARIANT THR-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE=92108420; Pubmed=1837174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRYSTALLOGRAPHY (2.8 ANGSTROMS).
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EMBL; M11234; AAA52122.1; -.
EMBL; M11220; AAA52578.1; -.
EMBL; X03021; CAA26822.1; -.
EMBL; M10663; AAA52121.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 254:1779-1782(1991).
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EMBO J. 4:2561-2568(1985)
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Gaps ; 0

Length 144; 0; Indels

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EMBL; EMBL; EMBL;

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76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
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      76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 APARLPSPGMQPWEHVNAIQEARRILINLSRDTAAEMNKTVEVVSEMFDLQEPSCVQTRLE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 144 granulocyte-macrophage colony-stimulating
factor precursor.
144 AA; 16220 MW; 2321CAE533040D04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 APARSPSPSTQPWEHTWAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
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01-DEC-1992 (Rel. 24, Last sequence update)
05-JUD-2004 (Rel. 44, Last annotation update)
Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
(Colony-stimulating factor) (CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=GM-CSF;

Papio anubis (Olive baboon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005129; F:granulocyte macrophage colony-stimulating f.,
GO; GO:0005129; F:granulocyte macrophage colony-stimulating f.,
GO; GO:0005055; P:jmmune response; IEA.
InterPro; IPR000773; 4 helix_cytokine.
InterPro; IPR000773; GM CSF.
PRINTS; PR00693; GMCSFACTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granulocyte-macrophage colony-stimulating factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Villinger F.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY234216; AAO85329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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92.1%; Pred. No. 7.4e-51;
tive 7; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom, PD007349; GM_CSF; 1.
SMART; SM00040; CSF2; 1.
PROSITE; PS00702; GM_CSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 92.1
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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144
                                                                                                                           136 CWEPVOE 142
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                                                                                                                                                                                138 CWEPVOE 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9555;
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01-JUN-2003 (
01-MAR-2004 (
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Ovis aries (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHEEP
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P28773;
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SIGNAL
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CSF2 SHEEP
TD CSF2 SI
AC P28773 SI
DT 01-DEC
DT 01-DEC
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DT 05-DEC
DT 05-DEC
ON Name=C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPBTSCATQIITFESFKENLKDFLLVIPFD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 LYKQGLRGSLTKLKGPLTWAASHYKQHCPPTPETSCATQTITFESFKENLKDFLLVIPFD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 APARSPSPSTOPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLOEPTCLOTRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21479645; PubMed=11596094; DOI=10.1002/jmv.2073.abs; Hutchinson K.L., Villinger F., Miranda M.E., Ksiazek T.G., Peters C.J., Rollin P.E.; Miranda M.E., Ksiazek T.G., "Multiplex analysis of cytokines in the blood of cynomolgus macaques naturally infected with Ebola virus (Reston serotype)."; J. Med. Virus. 65:561-56(2001).

EMBL, AX007376; AAG16626.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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GO, GO:0005576; C:extracellular; IEA.

GO; GO:000529; F:granulocyte macrophage colony-stimulating f.

GO; GO:0006525; P:immune response; IEA.

InterPro; IPR009073; GM CSF.

InterPro; IPR00073; GM CSF.

Pfam; PF01109; GM CSF, I.

PRINTS; PR00693; GM CSF, I.

PRODM; PD007349; GM CSF; I.

PROSITE; PS00702; GM CSF; I.

SRQUENCE 144 AA; I6177 MW; 7D5F38IDA2FC832F CRC64;
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                                                                                                                                                                                                                                                                                                                                                          Query Match 86.8%; Score 664; DB 2; Length 144; Best Local Similarity 98.4%; Pred. No. 9.8e-54; Matches 125; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                        Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                          1441; AAU21240.1; -.
144 AA; 16269 MW; 75D1E0B9D4D1A1A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Granulocyte-macrophage colony stimulating factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Granulocyte-macrophage colony-stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                    EMBL; AY720441; AAU21240.1; SEQUENCE 144 AA; 16269 MP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWEPVQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 CWEPVQE 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=GM-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
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Q9GL44
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Gaps

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Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 1
144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cervinae, Cervus
NCBI_TaxID=9860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
                 NCBI_TaxID=9940;
  Caprinae; Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=CSF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P51748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEREL
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  셤
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                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.
Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 APARSPSPSTQPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
                                                                                SEQUENCE FROM N.A.

MEDLINE=92039044; PubMed=1937025; DOI=10.1016/0378-1119(91)90163-6;

MCINES C.J., Haig M.C.K.;

"Cloning and expression of a cDNA encoding ovine granulocyte-
macrophage colony-stimulating factor.";

Gene 105:275-279(1991).

-I-FUNCTION: Cytokine that stimulates the growth and differentiation of hematopoietic precursor cells from various lineages, including granulocytes, macrophages, eosinophils and erythrocytes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
  Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Granulocyte-macrophage colony-stimulating factor (Fragment).
Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 548; DB 1; Length 144;
; Pred. No. 5.7e-43;
10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 By similarity.
138 By similarity.
4 N-linked (GLONAC. . .) (Pc
16318 MW; ABAAC8733BS80008 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P04141; 2GMF.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR000773; GM CSF.
Pfam; PF01109; GM CSF; 1.
PRINTS; PR06089; GMCSR-CTOR.
Pr000m; PD007449; GM CSF; 1.
SMART; SM00040; CSF2; 1.
SMART; SN00040; GSF2; 1.
Cytokine; Glycoprotein; Growth factor; Signal.
SIGNAL
                                                                                                                                                                                                                                                                           elmilarity).
-- SUBGELLULAR LOCATION: Secreted.
-- SUBCELLULAR: DOCATION: Secreted.
-- SIMILARITY: Belongs to the GM-CSF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X53561; CAA37632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CWEPVOK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                         NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
105
44
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                          Caprinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9MYK4;
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Q9MYK4
SOURCE CONTRACTOR OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 APTRQPSPVTRPWQHVDAIKEALSLLNDSTDTAAVMDETVEVVSEMFDSQEPTCLQTRLE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulocyte-macrophage colony-stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Cytokine that simulates the growth and differentiation of hematopoietic precursor cells from various lineages, including granulocytes, macrophages, eosinophils and erythrocytes (By
MEDLINE=91331592; PubMed=1869289; O'Brien P.M., Rothel J.S., Seow H.F., Wood P.R.; "Cloning and sequencing of the cDNA for ovine granulocyte-Macrophage colony stimulating factor (GM-CSF)."; Immunol. Cell Biol. 69:51-55(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
(Colony-stimulating factor) (CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cervus elaphus (Red deer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
                                                                                                                                                                                                                  O'Brien P.; Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
EMBL, X55991; CAA39463.1; -.
PIR, A61632; A61632.
HSSP, P04141; 2CMF.
GO, GO:0005576; C:extracellular; IEA.
GO, GO:0005129; Faranulocyte macrophage colony-stimulating f.
GO; GO:0006955; P:immune response; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16290 MW; ABAAD7633B580008 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%; Score 544; DB 2;
79.5%; Pred. No. 1.3e-42;
tive 10; Mismatches 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR009079; 4 helix_cytckine.
InterPro; IPR000773; GM_CSF.
Pfam; PF01109; GM_CSF; I.
PRINTS; PR00693; GMCSFACTOR.
ProDom; PD007349; GM_CSF; I.
SMART; SM00040; CSF2; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                  136 CWEPVQE 142
                                                                                                                                                                                                                                                                                                                                                                                                             138 CWKPAQK 144
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ID CSF2 PIG S
AC Q29118; Q29046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 CW 137
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Q95L10
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 LYKQGLRGSLTSLSGSLTMMARHYEQHCPPTQETSCETQTITFKSFKENLKDFLFIIFFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 APTRPASPUTRPWQHVDAIKEALSLINHSSDTAAVMNETVEVVSEMFDSQEPTCLQTRLK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
GO; GO:0005955; P:immune response; IEA.
GO; GO:001109; GM CSF; 1.
PRINTS; PR00693; GMCSF; 1.
PRODOM; PD007349; GM CSF; 1.
SMART; SM00040; CSF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vecchione A., D'Mello F., Kanellos T.S., Howard C.R., Hamblin A.S. Catchpole B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=GN-CSF;
Bquus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 By similarity.
138 By similarity.
44 N-linked (GlcNAc. .) (Potential).
54 N-linked (GlcNAc. .) (Potential).
16283 MW, 1F5FF5FD03C94394 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Granulocyte-macrophage colony-stimulating factor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF448481; AAL41017.2; -- HSSP; P04141; 2GMF.
                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00040; CSF2; 1.
PROSITE; PS00702; GM CSF; 1.
Cytokine, Glycoprotein; Growth factor; Signal.
SIGNAL 1 17 By similarity.
-!- SIMILARITY: Belongs to the GM-CSF family.
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                                                                                                                                                                                                                                               HSSP; P04141; 2GMF.

InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR000773; 4M CSF.

Pfam; PF01109; GM CSF; 1.

PRINTS; PR00693; GMCSFACTOR.
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                                                                                                                                                                                                                          EMBL; U14392; AAA21439.1; -.
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SEQUENCE FROM N.A.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 LYKQGLRGSLIKLEGPLTWMASHYKQHCPPTLETSCATQMITFKSFKKNLKDFLFEIPFD 137
                                                                                                                                                                                                                                              76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 APTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELTCLQTRLK
                                                                                                                                                                  16 APARSPSPSTQPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                          ö
                                                                                  Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 152;
                                                                           Query Match 68.9%; Score 527; DB 2; Length 14 Best Local Similarity 77.2%; Pred. No. 5.1e-41; Matches 98; Conservative 13; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.1%; Score 513; DB 2; Length 15
Best Local Similarity 78.7%; Pred. No. 1.1e-39;
Matches 96; Conservative 11; Mismatches 15; Indels
PROSITE; PS00702; GM_CSF; 1.
NON TER 146 146
SEQUENCE 146 AA; 16604 MW; B92D0617F391281C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Granulocyte-macrophage colony-stimulating-factor.
Name=GM-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA
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144 AA.

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144 AA; 16254 MW; 793DACB62CF736D0 CRC64;
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01-JUL-1989 (
05-JUL-2004 (
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1D CSF2 BOVIN

AC P11052;

DT 01-JUL-1989

DT 05-JUL-2004
      SEQUENCE
                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cho Y.W., Choi I.-S., Yoo H.S.;
"Cloning of porcine granulocyte macrophage-colony stimulating factor in alveolar macrophages.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that stimulates the growth and differentiation of hematopoletic precursor cells from various lineages, including granulocytes, macrophages, eosinophils and erythrocytes (By
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-VUL-2004 (Rel. 44, Last annotation update)
Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
(Colony-stimulating factor) (CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDILINES-96167041, PubMed=8595928;
Inumaru S., Takamatsu H.,
"CDNA cloning of porcine granulocyte-macrophage colony-stimulating
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                              Gloster S.E., Sandeman R.M., Strom A.D.G.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       Foss D.L., Murtaugh M.P.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pactor:
By similarity.
By similarity.
N-linked (GloNAc. .) (1)
N-linked (GloNAc. .) (2)
V -> I (in Ref. 2).
C -> E (in Ref. 2).
VK -> AQ (in Ref. 2).
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the GM-CSF family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AX116564; AAM48280.1; -.
HSSP; P04141; 2GMF.
HIGEPPO; IPRO00979; 4 helix_cytokine.
InterPro; IPR000979; 4 melix_cytokine.
InterPro; PR000973; 6W CSF.
Pfam; PF01109; GM CSF; I.
ProDom; PD007349; GM CSF; I.
SWART; SW00040; CSF2; I.
PROSITE; PS00702; GM_CSF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. Cell Biol. 73:474-476(1995).
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144
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                                                                                                                                    Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                  TISSUE=Spleen;
                                                                                                                Name=CSF2;
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                                                                                                            16 APARSPSFSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
                                                                                                                                           18 APTRPPSPVTRPWQHVDAIKEALSLINNSNDTAAVMNETVDVVCEMFDPQEPTCVQTRLN 77
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dhinakar Raj G., Harishankar M., Thennarasu S., Mahalinga Nainar A.; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, ANSS190; AASS9070.1; ...

GO; GO:0005576; C:=extracellular; IEA.

GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. ..; Interpro; IPR009073; GA helix.cytokine.

Interpro; IPR0090773; GA CSF.

PEam; PF01109; GM_CSF, T.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Granulocyte macrophage colony stimulating factor.
Bubalus bubalis (Domestic water buffalo).
Bukaryotas, Metazoa, Chordate, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bubalus.
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Length 144;
                                                      22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89; Conservative 18; Mismatches 19; Indels
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ProDom; PD007349; GM CSF; 1.
SMART; SM00040; CSF2; 1.
SROATTS; SM00702; GM CSF; 1.
SEQUENCE 143 AA; 16105 MW; 274532FF0FFE4C3F CRC64;
/ Match 63.7%; Score 487; DB 1; Local Similarity 70.1%; Pred. No. 2.6e-37; Nes 89; Conservative 16; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.6%; Score 486.5; DB 2 70.1%; Pred. No. 2.9e-37;
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(Rel. 11, Last sequence update)
(Rel. 44, Last annotation update)
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138 CWGPVKK 144
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136 CWEPVQE 142
137 CWEPAQK 143
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105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                       CANFA
                                                                                                                                                                                                                                                      Name=CSF2;
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 APARSPSPSTQPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 APTRPPNTATRPWQHVDAIKEALSLLNHSSDTDAVMNDT-EVVSEKFDSQEPTCLQTRLK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=90021093; PubMed=2678728; DOI=10.1016/0165-2427(89)90036-6;
Leong S.R., Flaggs G.M., Lawman M.J.P., Gray P.W.;
Leong S.R., Flaggs G.M., Lawman M.J.P., Gray P.W.;

"Cloning and expression of the cDNA for bovine granulocyte-macrophage colony-stimulating factor.";

Vet. Immunol. Immunol. 21:261-278(1989).

-!- FUNCTION: Cytokine that stimulates the growth and differentiation of hematopoietic precursor cells from various lineages, including granulocytes, macrophages, eosinophils and erythrocytes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                            MEDLINE=89096971; PubMed=3062386; DOI=10.1016/0161-5890(88)90120-4; Mallsazewski C.R., Schoenborn M.A., Cerretti D.P., Mignall J.M., Picha K.S., Cosman D., Tushinski R.J., Gillis S., Baker P.E.; "Bovine GM-CSF: molecular cloning and biological activity of the
Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF) (Colony-stimulating factor) (CSF).
                                                           Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
N-linked (GlcNac. .) (Potential)
N-linked (GlcNac. .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.8%; Score 480.5; DB 1; Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4A24E26A870A51EC CRC64;
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SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the GM-CSF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P04141; 2GMF.
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR000773; GM_CSF.
Ffan; PF01109; GM_CSF; I.
PRINTS; PR00693; GMCSFACTOR.
PRODOM; PD007349; GM_CSF; I.
PROSITE; SMO0040; CSF2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16157 MW;
                                                                                                                                                                                                                                                                                                                    Mol. Immunol. 25:843-850(1988)
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PIR; JL0037; FQBOGM.
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                                                                                                                                                                                                                                                                                                recombinant protein."
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                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=9913;
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44
54
                                                                                                                             Bovinae; Bos
                                         Name=CSF2;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Cytckine that stimulates the growth and differentiation of hematopoietic precursor cells from various lineages, including granulocytes, macrophages, eosinophils and erythrocytes (By
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                                                                                                                                                Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF) (Colony-stimulating factor) (CSF).
                                                                                                                                                                                                                                                             Canib iamiliaile (JOSJ).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91329842; PubMed-1868252;
Nash R.A., Schuening F., Appelbaum F.R., Hammond W.P., Boone T.,
Morris C.F., Slichter S.J., Strob R.;
"Molecular cloning and in vivo evaluation of canine granulocyte-
macrophage colony-etimulating factor.";
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68.5%; Pred. No. 5.2e-36;
ive 19; Mismatches 21; Indels
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By similarity.
N-linked (GlcNAc. . .) (P. 6323807E1F1C6343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01109; GM CSF; I.
PRINTS; PR00693; GMCSFACTOR.
ProDom; PD007349; GM CSF; 1.
SMART; SM00040; CSF2; 1.
Cytokine; Glycoprotein; Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the GM-CSF family.
                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
144 AA
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InterPro, IPR009079; 4_helix_cytokine.
InterPro, IPR000773; GM_CSF.
PRT;
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Best Local Similarity 68.5'
Matches 87; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78:930-937(1991).
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138
                                                                                                                                                                                                                                          Canis familiaris (Dog)
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Job time : 179 secs
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                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR000773; GM_CSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 APARSPSPSTQPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes K.J., O'Reilly K.L.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that stimulates the growth and differentiation
of hematopoietic precursor cells from various lineages, including
granulocytes, macrophages, eosinophils and erythrocytes (By
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 44, Last annotation update)
Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
(Colony-stimulating factor)
                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Granulocyte-macrophage colony-stimulating factor (Fragment).
Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 472; DB 2; Length 141;
; Pred. No. 6.2e-36;
14; Mismatches 25; Indels
                                                                                                                                                                                                                                Dunham S.P., Bruce J., Jarrett O.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX138140; AAN11308.1; --
HSSP; P04141; ICSG.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 141 AA; 16039 MW; D7E78E3DA77C1F66 CRC64;
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000773; GM CSF; I.
ProDom; PD007349; GM CSF; I.
SMART; SM00040; CSF; I.
PROSITE; PS00702; GM CSF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                          61.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 69.39
Matches 88, Conservative
                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
||:||::
138 CWKPVKK 144
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|35 CWKPVQK 141
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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062757;
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                                                  RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQITTFESFKENLKDFLLVIPFD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 APTSSPSSVTRPWQHVDAMKEALSLINNSSEITAVMNETVEVVSEMFDPEEPKCLQTHLK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
Granulocyte-macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.

By similarity.

By similarity.

N-linked (GlcNAc. . .) (Potential)

N-linked (GlcNAc. . .) (Potential)

N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42C5BF5F8235DA55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.0%; Score 451; DB 1;
66.9%; Pred. No. 5.7e-34;
iive 14; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n, Growth factor; Signal.
-!- SIMILARITY: Belongs to the GM-CSF family.
                                                                                                                                                                                                                                                                                                          HSSP; P04141; 2GMP.

InterPro; IPR009079; 4 helix_cytokine.

InterPro; IPR000773; GM CSF.

Pfam; PF01109; GM CSF; I.

PRINTS; PR00693; GMCSFACTOR.

ProDom; PD007349; GM_CSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 8, 2005, 16:13:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 N-
54 N-
16505 MW;
                                                                                                                                                                                                                                                                               EMBL; AF053007; AAC06041.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.9
nes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00040; CSF2;
PROSITE; PS00702; GM
Cytokine; Glycoprotei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 CWEPVQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CWGPDOK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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8, 2005, 15:55:38 ; Search time 164 Seconds (without alignments) 334.878 Million cell updates/sec protein search, using sw model March OM protein Run on:

765 1 MHHHHHHSSGIEGRMAPARS......BNLKDFLLVIPFDCWEPVQE 142 US-10-723-083-2 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: *
geneseqp2000s: *
geneseqp2000s: *
geneseqp2001s: *
geneseqp2001s: *
geneseqp2003s: *
geneseqp2003bs: * Genesed 16Dec04:* Database

Pred? No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ai	Description
	682	89.2	259	2	AAR79317	Aar79317 IL-3 cont
7	682	89.2	259	m	AAY53198	Aay53198 Human int
٣	682	89.2	259	4	AAE13992	Aael3992 Myelopoie
4	682	89.2	259	'n	ABG97765	9
ហ	682	89.2	259	ω	ADJ14353	е
9	619	88.8	533	~	AAW19763	Aaw19763 p53-GM-CS
7	678	88.6	128	щ	AAP90118	Aap90118 Synthetic
8	678	88.6	128	Н	AAP90115	
6	678	88.6	128	7	AAR79338	Aar79338 pMON13012
10	678	88.6	128	7	AAW00103	Aaw00103 Granulocy
11	678	88.6	128	m	AAY53217	Aay53217 Human G-C
12	678	88.6	128	4	AAE14011	Aae14011 Chemicall
13	678	988.	128	2	ABG97784	Abg97784 Human Int
14	678	88.6	128	œ	ADJ14372	
15	678	88.6	274	~	AAR79320	Aar79320 IL-3 cont
16	678	88.6	274	m	AAY53201	Aay53201 Human int
17	678	88.6	274	4	AAE13995	Aae13995 Myelopoie
18	678	88.6	274	2	ABG97768	_
19	678	88.6	274	80	ADJ14356	Adj14356 Chimera p
20	678		301	7	AAR79318	Aar79318 IL-3 cont
21	678	8	301	٣	AAY53199	Aay53199 Human int
22	678	98.6	301	4	AAE13993	Aae13993 Chemicall
23	678		301	Ŋ	ABG97766	Abg97766 Human Int
24	919	88.4	523	m	AAY44994	Aay44994 HD70scFv-
25	675	88.2	712	8	ADL16720	Adl16720 Human stu

Adf15029 Human alb	Adf14935 Human alb	Adf14936 Human alb	Aar03199 New human	Aar13215 Oxidised	Aar41540 r-h-GM-CS	Aay69025 Amino aci	Aael3117 Mature hu	Abb78399 Amino aci	Adf70845 Human mac	Adl88868 Human cyt	Aaw00102 Granulocy	Aap70351 Sequence	Abb08135 Human GMC	Abg31632 Human gra	Aao19090 Human gra	Adj36195 Self-coal	Aap60418 Human gra	Aap70657 Sequence	Aar04098 Metapyroc	
ADF15029	ADF14935	ADF14936	AAR03199	AAR13215	AAR41540	AAY69025	AAE13117	ABB78399	ADF70845	ADL88868	AAW00102	AAP70351	ABB08135	ABG31632	AA019090	ADJ36195	AAP60418	AAP70657	AAR04098	
_	^	7	N	~	~	m	4	S	7	œ	0	Н	Ŋ	ß	Ŋ	Φ	-	M	7	
736	736	736	128	127	127	127	127	127	127	127	128	131	131	131	131	143	144	144	144	
88.2	88.2	88.2	88.1	88.0	98.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0	
675	675	674.5	674	673	673	673	673	673	673	673	673	673	673	673	673	673	673	673	673	
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

AAR79317 standard; protein; 259 AA. (first entry) 25-AUG-1999 AAR79317; RESULT 1 AAR79317

IL-3 containing fusion protein.

CSF; colony stimulating factor; cytokine; lymphokine; interleukin; hIL-3; CSF; colony mutant; mutein; fusion protein.

Synthetic.

WO9521254-A1. 10-AUG-1995.

95WO-US001185. 02-FEB-1995;

94US-00192325 04-FEB-1994;

(SEAR) SEARLE & CO G D.

Easton AM; Caparon MH, Thomas JW; Braford-Goldberg SR, Olins PO, Paik K, Abrams MA, Mckearn JP, Bauer CS, Klein BK,

WPI; 1995-283774/37. N-PSDB; AAQ97169.

and Fusion proteins comprising a human interleukin-3 variant, a linker e interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.

Claim 16; Page 86; 447pp; English

A new fusion protein has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, in which R1 is a mutant or variant of human interleukin-3 (h1L-3) having the present generic sequence. R2 is a second colony stimulating factor (GSP) including cytokine, lymphokine, interleukin, haematopoietic growth factor or IL-3 variant, and L is a linker. The present sequence corresponds to all-3 variant, and L is a linker. The present sequence corresponds to Learnich H1L-3(1-133) in which 1-14 amino acids may be deleted from the N-terminal, 1-15 amino acids can be deleted from the N-terminal, 1-15 amino acids in the region 17-123 are different from those in the native protein. The fusion protein is used to increase haematopoietic cell production. It is also useful as an IL-3 antagonist or as a discrete antigenic fragment for

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Antagonists are used to block the growth of certain cancer cells and intreatment of asthma. The fusion protein can also be used to stimulate bone marrow and blood cell activation and growth in vitro before infusion erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic system. The protein has the usual activity of both its component undesired side effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 SGGSNWAPARSPSPSTQPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQ11TPESFKENLKDF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutated
other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGIEGRMAPARSPSPSTOPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine; colony stimulating factor; haematopoietic growth factor; lymphokine; fusion protein; haematopoietic disorder; infection; cancer; radiation therapy; chemcherapy, bone marrow suppressive drug; bone marrow activation; blood cell activation; blood transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human interleukin-3 mutant containing fusion protein SEQ ID NO:141.
production of antibodies useful in immunoassays and immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating hematopoietic disorders with fusion proteins comprising interleukin-3 fused with secondary colony stimulating factors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                      Score 682; DB 2; Length 259;
Pred. No. 2.2e-64;
0; Mismatches 4; Indels
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Caparon MH;
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Paik K, Thomas JW, Mckearn JP, Olins PO,
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95WO-US001185.
95US-00411795.
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 97.0%;
Matches 130; Conservative
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                                                                                                                                                                                                                                                                                                                          Sequence 259 AA;
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02-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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AAYS3198
AAXS3198
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stimulating factors (CSPS) (e.g. cytokines, lymphokines, interleukin.

catalor haematopoletic colony stimulating factors) or other interleukin.

cardor haematopoletic colony stimulating factors) or other interleukin.

cardor haematopoletic colony stimulating factors or other interleukin.

cardor haematopoletic disorders resulting from bacterial, viral and fungal infections, cancer radiation therapy, chemotherapy or bone marrow suppressive drugs. They may also be used in vitro to stimulate bone marrow and blood call activation and growth prior to infusion of the bone marrow and blood transplants into patients. IL-3 is a haematopoietic marrow and blood transplants into patients. IL-3 is a haematopoietic colls. The fusion coll constituent peptides and further by having a biological or by physiological activity greater than the additive function of the IL-3 or second CSF alone (1.e. the peptides act synergistically). Their activity may also be further enhanced by the mutations they comprise. The variations may further reduce undesirable side effects associated with IL car and AAAA3722 to AAAA03782 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; virucide; interleukin-3; IL-3; haematopoietic disorder; haematopoietic growth factor receptor; neutropenia; thrombocytopenia; leukopenia; anaemia; chemotherapy; bone marrow transplantation; burn; radiation therapy; haematopoietic progenitor mobilisation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 CLOTRLELYKOGLRGSLTKLKCBVTWMASHYKOHCPPTPETSCATOIITFESFKENLKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.2%; Score 682; DB 3; Length 259; Best Local Similarity 97.0%; Pred. No. 2.2e-64; Matches 130; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE13992 standard; protein; 259 AA
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NICASTRO P.
QI H.
SEDO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FINN R.
GOKARN Y.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 259 AA;
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(FINN/) I
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(OIHH/)
(SEDO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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  SXR
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                                                                                                                                                                                                                                                                                      The invention relates to chemically modified myelopoietin (MPO) conjugates having at least one water-soluble polymer molecule covalently attactivating group, to at least one amino acid residue of a biologically active myelopoietin polypeptide. MPOS are multifunctional agonists of human interleukin-3 (IL-3) and another haematopoietic growth factor receptor. Sequences of the invention are useful for treating haematopoietic disorders (e.g. neutropenia, leukopenia, thrombocytopenia and anaemia), including those arising from chemotherapy and radiation therapy. MPOs are also useful in bone marrow transplantation, wound healing, burn treatment and the treatment of parasite, bacterial or viral infection. They are useful for mobilising haematopoietic progenitors and stem cells. The chemically modified MPOS have a longer lasting neutrophil stem cells. The chemically modified MPOS have a longer lasting neutrophil decreased antigenicity than unmodified myelopoietins. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; interleukin-3; IL-3; mutant; mutein; stem cell; haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; G-CSF; G-CSFser17; c-mpl ligand; TPO; MGDF; errythropoietin; flt3 ligand; human growth hormone; B-cell growth factor; leukaemia; B-cell differentiation factor; cosinophil differentiation factor; transcription factor; ensuropenia; aplatic anaemia; thrombocycopenia; idiopathic neutropenia; chediak Higashi syndrome; systemic lupus erythematosus; SLE; myelodysplastic syndrome;
                                                                                                                                                                                  Myelopoietin conjugate for treating e.g. leukopenia comprises a water-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT
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                                                                  Siegel N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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Pred. No. 2.2e-64;
0; Mismatches 4; Indels
                                                                    Sedo K,
                                                                  Qi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Interleukin-3 chimaeric protein #20.
                                                                  Gokarn Y, Hills R, Nicastro P,
                                                                                                                                                                                                          soluble polymer attached to the protein.
                                                                                                                                                                                                                                                5; Page 197-198; 429pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG97765 standard; protein; 259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.0%;
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
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                                                                                                                                     WPI; 2001-657130/75
(SIEG/) SIEGEL N. (WALT/) WALTER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myelofibrosis.
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                                                                                     Walter S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                  Finn R,
                                                                                                                                                                                                                                                  Claim
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ABG97765
  THE SECOND SECON
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The invention relates to ex vivo expansion of stem cells, comprises culturing stem cells with a growth medium comprising a chimaera protein, and harvesting the cultured stem cells. The chimaera is based on a mutated human interleukin-3 (IL 3) sequence coupled to a haematopoietic factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-CSFS-17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16, IL 3 ligand, human growth hormone, B-cell growth factor, B-cell differentiation factor, eosinophil differentiation factor and stem cell factor (SCF) via a peptide linker. The formula for the chimaera is given in the specification. Also included is a method for enhancing the in the specification. Also included is a method for enhancing the chimaera is given in the specification of cultured stem cells by a heterologous gene, comprising; (a) removing stem cells from a patient or donor; (b) culturing the stem cells with a growth medium comprising the transduced cells; and (d) harvesting the transduced cells; and (d) harvesting the transduced cells; and centaring the efficiency of the transduction of cultured stem cells by a heterologous gene. The method is also useful for treating a patient cells are also useful in the treatment of cyclic neutropenia, aplaetic anaemia, thrombocytopenia, idiopathic entropenia, chediak-Higdshi synforme, thrombocytopenia, idiopathic entropenia, chediak-Higdshi synforme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systemic lupus erythematosus (SLB), leukaemia, myelodysplastic syndrome and myelofibrosis. The present sequence is a human IL-3 mutant/haematopoietic factor chimaeric sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ex vivo expansion of stem cells, for enhancing transduction efficiency cultured stem cells, comprises culturing stem cells in growth medium having mutant interleukin-3, and hematopoietic factor, and harvesting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 SGCGSNMAPARSPSPSTQPWEHVNAIQBARRLLNLSRDTAAEMNETVEVISEMFDLQEPT
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                                                                                                                                                                                                                                                                                                                                                                                                  Easton AM;
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                                                                                                                                                                                                                                                                                                                                                                                               Caparon MH,
Thomas JW;
                                                                                                                                                                                                                                                                                                                                                                                               Braford-Goldberg SR,
Olins PO, Paik K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Col 247-250; 203pp; English.
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                                                                                             93WO-US011197.
94US-00192325.
95WO-US001185.
95US-00411795.
96US-00762227
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Mckearn JP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cultured cells.
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                                                                                                                                                                     04-FEB-1995;
06-APR-1995;
06-JUN-1995;
09-DEC-1996;
                                                                                                         22-NOV-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                           Bauer SC,
Klein BK,
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20-MAY-2004 (first entry)
                                                                                                                                              WPI; 2004-096775/10.
                                                                                                                         PAIK K.
THOMAS J W.
                                                                                                                                                                                                                            Sequence 259 AA;
                                               US2003185790-A1
                                                            26-FEB-2002;
                                        Unidentified
                                                      02-OCT-2003
                                                                   24-NOV-1992
22-NOV-1993
                                                                          04-FEB-1994
                                                                                 06-APR-1995
06-JUN-1995
                                                                                        09-DEC-1996
                                                                                                                                    Bauer SC,
Klein BK,
                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 130,
                                                                                                                      (OLIN/)
(PAIK/)
(THOM/)
                                                                                               BAUE/)
                                                                                                               (KLEI/)
(MCKE/)
                                                                                                        (CAPA/)
                                                                                                  ABRA/
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A fusion protein (AAM19763) comprises human p53 tumour suppressor protein and granulocyte-macrophage colony stimulating factor (GM- CSF). It is the expression product of a nucleic acid molecule (AAT72724) prepd. by PCR amplification of p53 cDNA GM-GSF DNA sequences (the GM-CSF antisense primer including a hexahistidine tag sequence) and their fusion via a AbaI linker. Fusion expression vectors can be used to transfect mammalian and insect cells. The p53-GM-GSF fusion protein is used to generate anti-p53 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen- presenting cells exposed to the fusion protein
126 SGGGSNWAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response in a vertebrate
                                                                                186 CLÓTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF
                                           CLOTRLELYKOGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53-GM-CSF; granulocyte macrophage colony stimulating factor; tumour suppressor gene; immunostimulant; cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Xbal linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525. .533
/note= "hexahistidine tag"
                                                                                                                                                                                                                                                                                                                                                                                                                         p53-GM-CSF immunostimulant fusion protein.
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                                                                                                                                                                                                                                                                                           AAW19763 standard; protein; 533 AA
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/label= p53
394. .395
/label= Linker
/note= "product o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Fig 11; 45pp; English.
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/label= GM-CSF
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                                                                                                                                   LLVIPFDCWEPVQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT72724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method whereby stem cells are ex vivo expanded via culturing the stem cells with a growth medium comprising a chimera protein, followed by harvesting of the cultured stem cells. The method of the invention has antianaemic, immunostimulant, immunosuppressive, cytostatic and neuroprotective applications and may be useful to target haemopoietic cells for gene therapy, preferably for treating patients having a haemopoietic disorder characterised by decreased levels of having a haemopoietic disorder characterised by decreased levels of having a haemopoietic and/or megakarycyte cells of haemopoietic system. The expanded ex vivo cells may be used to treat neutropenia, aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome, aplastic anaemia, periodic neutropenia, myelodishersis syndrome or myelofibrosis. The current sequence is that of a chimera protein related to the human interleukin-3 (IL-3) mutant protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                            stem cell; antianaemic; immunostimulant; immunomodulator; antiinflammatory; dermatological; immunosuppressive; cytostatic; antiinflammatory; haemopoietic disorder; gene therapy; myeloid; erythroid; lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia; chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia; myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; chimera.
                                                                     Chimera protein related to human interleukin-3 mutant protein SEQ ID 141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating aplastic anemia, involves culturing the stem cells with growth medium comprising chimera protein, and harvesting the cultured stem cells.
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Thomas JW;
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Olins PO, Paik K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 141; 202pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABRAMS M A.
BRAFORD-GOLDBERG S R.
CAPARON M H.
BASTON A M.
KLEIN B K.
MCKEARN J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00981044.
93WO-US011197.
94US-00192325.
95WO-US001185.
95US-00446872.
96US-00762227.
                                                                                                                                                                                                                                                                                                                                                                                                       2002US-00083446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Mckearn JP,
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Length 533;

Score 679; DB 2; Pred. No. 1.3e-63;

88.88; 97.78;

Query Match Best Local Similarity

68

9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT

sal Similarity 130; Conserv

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us-10-723-083-2.rag

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Matches

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61 ELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120
                                                                                                                                                                                                                                        Human granulocyte colony stimulating factor; Synthetic restriction sites; cassette mutagenesis; GM-CSF; expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human granulocyte-macrophage colony stimulating factor - synthetic DNA includes restriction sites for cassette mutagenesis and incorporation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic human granulocyte colony stimulating factor (GM-CSF), see corresp. AAN90274. Its DNA has useful restriction sites for: HindIII; BspMi; NcoI; BstEII; BsmI; EcoRV; BgII; ApaI; Ball; XmnI; BamHI; and EcoRI. Used to facilitate cassette mutagenesis of selected regions. Synthesised by phosphoramidite chemistry, by dividing desired gene into 18 oligomers. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPARSPSPSTQPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
                                                                                                                                                                                                             Synthetic human granulocyte colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 678; DB 1; I
Pred. No. 2.3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                               AAP90115 standard; protein; 128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 3a; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        87GB-00026580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRBI-) BRITISH BIO-TECHN L.
                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128; Conservative
||||||||||||||
DCWEPVQE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-208958/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCWEPVQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 128 AA;
                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1987;
                                                                                                                                                            25-MAR-2003
01-NOV-1989
                                                                                                                                                                                                                                                                                                                                          GB2212159-A
                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edwards RM;
                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 128
                                                                                                                              AAP90115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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                  121
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                                                            RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic human granulocyte colony stimulating factor (GM-CSF) contg. useful restriction sites, and a BspMI site. See corresp. AAN90383. Its DNA is useful for generating blunt ends in fusion protein prodn. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                  512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                               TRLELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
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                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recognition site for BspMI enzyme - allowing generation of fusion in prodn. of fusion proteins.
                                                                                                               TRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESPKENLKDFLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPARSPSPSTQPWEHVNAIQEARRILINISRDIAAEMNETVEVISEMFDLQEPTCLQTRI
                                 EGRMAPARSPSPSTQPWEHVNAIQEARRILINLSRDTAAEMNETVEVISEMFDLQEPTCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 MAPARSPSPSTQPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       BspMI; restriction sites; blunt ends; fusion proteins; synthetic;
human granulocyte colony stimulating factor.
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic human granulyte colony stimulating factor.
 2;
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Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 128; Conservative 0; Mismatches 0;
 Mismatches
                                                                                                                                                                                                                                                                         AAP90118 standard; protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 2; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87GB-00026581
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRBI-) BRITISH BIO-TECHN
                                                                                                                                                            142
 Conservative
                                                                                                                                                                                           IPFDCWEPVQE 523
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                                                                                                                                                            IPFDCWEPVOE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN90383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA including
blunt end for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                      01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB2212160-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edwards RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                         513
                                 12
                                                             393
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A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1, CR1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF) including cytokine, 1ymphokine, interleukin, haematopoietic growth factor or IL-3 variant, and L is a linker. Generic sequences are described in AAW03235 - AAW03242, and specifically claimed examples are shown in CC AAR793428 R79335 and AAR79342-T79345. The fusion protein is made by recombinant DNA techniques. Specifically claimed examples of DNA cequences which encode these proteins are shown in AAQ97167-Q97204 and AAQ9722-C99727. The fusion protein is used to increase haemactopoietic cell production. It is also useful as an IL-3 antagonist or as a discrete antigenic fragment for production of antibodies useful in immunoassays and immunotherapy. Antagonists are used to block the growth of certain can end immunotherapy. Antagonist are used to block the growth of certain can end in immunoassay of the object of myeloid, erythroid, lymphoid and/or megakarycyce cells of myeloid, erythroid, lymphoid and/or megakarycycyce cells of the haematopoietic system. The protein has the usual activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 BLYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPARSPSPSTQPWEHVNAIQEARRILINLSRDIAAEMNETVEVISEMFDLQEPICLQTRL 60
                                                                      CSF; colony stimulating factor; cytokine; lymphokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion proteins comprising a human interleukin-3 variant, a linker and interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 MAPARSPSPSTOPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
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                                                                                                                                                                                                                                                                                                                                                                             Easton AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                           Braford-Goldberg SR, Caparon MH,
Olins PO, Paik K, Thomas JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 100.0%; Pred. No. 2.3
Matches 128; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 20; Page 125; 447pp; English.
                                                                                              mutant; mutein; fusion protein
                                                                                                                                                                                                                                                               95WO-US001185.
                                                                                                                                                                                                                                                                                                    94US-00192325.
25-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                          (SEAR ) SEARLE & CO G D.
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                                                                                                                                                                                                                                                                                                                                                                             Abrams MA,
Mckearn JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCWEPVOE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-283774/37.
N-PSDB; AAQ97208.
                                                                        Interleukin; hIL-3;
                                       pMON13012 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 128 AA;
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                        WO9521254-A1.
                                                                                                                                                                                                                                                                 02-FEB-1995;
                                                                                                                                                                                                                                                                                                      04-FEB-1994;
                                                                                                                                                                                                                              10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                               Bauer CS,
Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
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75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of human granulocyte macrophage colonystimulating factor (hGM-CSF; n = 101, Ile). A series of oligonucleotides were synthesised and ligated together to form a stable expression construct. The technique is used for the efficient prodm. of a glycoprotein with hGM-CSF activity. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAPARSPSPSTQPWEHVNAIQBARRILINLSRDTAAEMNBTVEVISEMFDLQEPTCLQTRL
                                                                                                                                                                                                                                                                                                                                                                                                    Prodm. of human granulocyte macrophage colony-stimulating factor - by culturing E. coli transformed with human GM-CSF DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 MAPARSPSPSTOPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
                                                                                                                         GM-CSF; granulocyte macrophage colony-stimulating factor; expression; construct; stable; production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
colony stimulating factor; haematopoietic growth factor; lymphokine;
fusion protein; haematopoietic disorder; infection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
                                                                                                 Granulocyte macrophage colony-stimulating factor (Ile101).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human G-CSF mutant protein sequence SEQ ID NO:160.
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100.0%; Pred. No. 2.3e-64
iive 0; Mismatches 0
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AAW00103 standard; protein; 128 AA.
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                                                                                                                                                                                                                                                           95JP-00263370.
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                                                      (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
(KIRI ) KIRIN BREWERY KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 DCWEPVQE 142
                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-365600/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DCWEPVQE
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT34400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 128 AA;
                                                                                                                                                                                                      JP08173185-A.
                                                                                                                                                                                                                                                             28-APR-1987;
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                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                09-JUL-1996.
                                                        25-MAR-2003
11-FEB-1997
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                           AAW00103;
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RESULT 10

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Methods have been developed for treating haematopoietic disorders with fusion proteins comprising recombinant, mutated human interleukin-3 (HIL-3) variants or mutant proteins (muteins) fused with secondary colony stimulating fused with secondary colony stimulating fused with secondary colony stimulating factors) or other interleukin-3 and/or haematopoietic colony stimulating from bacterial, viral and fungal creat hematopoietic disorders resulting from bacterial, viral and fungal infections, cancer radiation therapy, chemotherapy or bone marrow and blood cell activation and growth parior to stimulate bone marrow and blood cell activation and growth prior to infusion of the bone marrow and blood transplants into patients. IL-3 is a haematopoietic growth factor which has the property of being able to promote the marrow and blood transplants into patients. IL-3 is a haematopoietic growth factor which has the property of being able to promote the molecules are characterised by possessing the usual activity of both of their constituent peptides and further by having a biological or physiological activity greater than the additive function of the IL-3 or physiological activity greater than the additive function of the IL-3 or second CSF alone (i.e. the peptides act synergistically). Their activity may also be further reduce undesirable side effects associated with IL-3 AAYS3130 to AAYS3121 to AAAO3721 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating hematopoietic disorders with fusion proteins comprising mutated interleukin-3 fused with secondary colony stimulating factors or other interleukin-3 variants.
                                                                                                                                                                                                                                                                                                                                                                          Klein BK
radiation therapy; chemotherapy; bone marrow suppressive drug; bone marrow activation; blood cell activation; blood transplant.
                                                                                                                                                                                                                                                                                                                                                                        Easton AM,
Caparon MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                      Braford-Goldberg SR,
ckearn JP, Olins PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 20; Col 109-111; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Mckearn JP,
                                                                                                                                                                                                                                            94US-00192325.
95WO-US001185.
95US-00411795.
                                                                                                                                                                                                          95US-00469318.
                                                                                                                                                                                                                                                                                                                                (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                                                                                                          Abrams MA,
                                                                                                                                                                                                                                                                                                                                                                    f SC, Adlam.
K. Thomas JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-160368/14.
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                                                             Homo sapiens.
Synthetic.
                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                   04-FEB-1994;
                                                                                                                                                                                                                                                                      02-FEB-1995;
06-APR-1995;
                                                                                                                           US6022535-A
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                                                                                                                                                                                                                                                                                                                                                                                              Paik K,
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61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120
                                                                                                           ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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                                                                                   1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
                                                        MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
                              Gaps
                              ;
0
    Length 128;
                              0; Indels
    Score 678; DB 3; 1
Pred. No. 2.3e-64;
           100.0%; Pred. w..
    88.6%;
Query Match
Best Local Similarity 100.
Matches 128; Conservative
                                                                                                                                                                                 DCWEPVQE 142
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AAE14011 standard; protein; 128 AA.

RESULT 12 AAE14011 ID AAE

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conjugates having at least one water soluble polymer molecule covalently attached, via activating group, to at least one amino acid residue of a biologically active myelopoietin polypetide. MPOs are multifunctional agonists of human interleukin-3 (IL-3) and another haematopoietic growth factor receptor. Sequences of the invention are useful for treating haematopoietic disorders (e.g. neutropenia, leukopenia, thrombocytopenia and anaemia), including those arising from chemotherapy and radiation therapy. MPOs are also useful in bone marrow transplantation, wound healing, burn treatment and the treatment of parasite, bacterial or viral infection. They are useful for mobilising haematopoietic progenitors and stem cells. The chemically modified MPOs have a longer lasting neutrophilitelessing activity, decreased clearance rate, increased stability and decreased antigenicity than unmodified myelopoietins. The present sequence is a chemically modified myelopoietins. The present
                                                                                                               Myelopoietin conjugate, MPO, immunosuppressive, vulnerary, antiparasitic, antibacterial, virucide, interleukin-3; IL-3; haematopoietic disorder, haematopoietic growth factor receptor; neutropenia, thrombocytopenia, leukopenia, anaemia, chemotherapy, bone marrow transplantation; burn; radiation therapy, haematopoietic progenitor mobilisation; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 ELYKOGLRGSLIKLKGPLIMMASHYKQHCPPTPBTSCATQIITPESFKENLKDFLLVIPF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myelopoietin conjugate for treating e.g. leukopenia comprises a water-soluble polymer attached to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPARSPSPSTQPWEHVNAIQEARRILINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
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                                                                                 Chemically modified myelopoietin (MPO) conjugate related protein #11.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.6%; Score 678; DB 4; Length 128; 100.0%; Pred. No. 2.3e-64; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sedo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9i
H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 215; 429pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gokarn Y, Hills R,
                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000; 2000US-0195496P.
                                                                                                                                                                                                                                                                                                                                         06-APR-2001; 2001WO-US011256.
                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                           PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-657130/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NICASTRO P
                                                                                                                                                                                                                                                                                                                                                                                                                           FINN R.
GOKARN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEDO K.
SIEGEL N.
WALTER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HILLS R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 128 AA;
                                                                                                                                                                                                                                                                      WO200176639-A2.
                                                                                                                                                                                                   wound healing
                                                                                                                                                                                                                                      Unidentified.
                                               26-FEB-2002
                                                                                                                                                                                                                                                                                                        .8-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walter S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
               AAE14011;
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(SEDO/)
(SIEG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (GOKA/)
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Gaps

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0; Indels

Length 128;

Score 678; DB 5; 1 Pred. No. 2.3e-64;

134 9

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ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120
                               also useful in the treatment of cyclic neutropenia, aplastic anaemia, thrombocytopenia, idiopathic neutropenia, Chediak Higashi syndrome, systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome and myelofibrosis. The present sequence is a human IL-3 mutant/haematopoietic factor chimaeric sequence
having a haematopoietic disorder. The expanded haematopoietic cells are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPARSPSPSTQPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPTCLQTRL
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                                                                                                                                                                                                                                                                                  88.6%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
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nes 128; Conservative
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                                                                                                                                                                                                                                           Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003185790-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ex vivo expansion of stem cells, for enhancing transduction efficiency of cultured stem cells, comprises culturing stem cells in growth medium having mutant interleukin-3, and hematopoietic factor, and harvesting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; interleukin-3; IL-3; mutant; mutein; stem cell;
haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; G-CSF;
G-CSFSerl7; c-mpl ligand; TPO; MGDF; errythropoietin; flt3 ligand;
human growth hormone; B-cell growth factor; leukaemia;
B-cell differentiation factor; eosinophil differentiation factor;
stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
systemic lupus erythematosus; SLE; myelodysplastic syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Easton AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caparon MH,
Thomas JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Braford-Goldberg SR,
Olins PO, Paik K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Interleukin-3 chimaeric protein #39.
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                                                                                                                                                                                                                                                                    ABG97784 standard; protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-00981044.
93WO-US011197.
94US-00192325.
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95US-00411795
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Mckearn JP,
                                   142
                                                                                               121 DCWEPVOE 128
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                                   DCWEPVOE
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04-FEB-1994;
04-FEB-1995;
06-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2002
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Klein BK,
                               135
                                                                                                                                                                                                                                                                                                                                          ABG97784;
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erythroid;
                                                                                                                                                                                             Protein related to human interleukin-3 (IL-3) mutant protein SEQ ID 140.
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                                                                                                                                                                                                                                                        stem cell; antianaemic; immunostimulant; immunomodulator; antiinflammatory; dermatological; immunosuppressive; cytostatic; antionfortective; haemopoiatic disorder; gene therapy; myeloid; erytlymbhoid; megakaryocyte; aplastic anaemia; periodic neutropenia; Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia; myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caparon MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas JW;
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Olins PO, Paik K,
ADJ14372 standard; protein; 128 AA.
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93WO-US011197.
94US-00192325.
95WO-US001185.
95US-00411795.
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CAPARON M H.
                                                                                                                                  (first entry)
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Mckearn JP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EASTON A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLEIN B K.
MCKEARN J B
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THOMAS J W
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Klein BK,
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(OLIN/)
(PAIK/)
(THOM/)
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(BRAF/)
(CAPA/)
(EAST/)
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The invention relates to a novel method whereby stem cells are ex vivo expanded via culturing the stem cells with a growth medium comprising a chimera protein, followed by harvesting of the cultured stem cells. The method of the invention has antiansemic, immunostimulant, immunosuppressive, cytostatic and neuroprotective applications and may be useful to target haemopoietic cells for gene therapy, preferably for treating patients having a haemopoietic disorder characterised by decreased levels of maving a haemopoietic disorder characterised by decreased levels of paving a haemopoietic disorder characterised by decreased levels of system. The expanded ex vivo cells may be used to treat neutropenia, aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome, aplastic anaemia, periodic neutropenia, myelodysplastic syndrome or myelofibrosis. The current sequence is that of a protein related to the human interleukin-3 (IL-3) mutant protein of the invention.
                                           Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating aplastic anemia, involves culturing the stem cells with growth medium comprising chimera protein, and harvesting the cultured stem cells.
                                                                                                                                            Disclosure; SEQ ID NO 160; 202pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 128 AA;
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ELYKQCIRGSLTKIKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENIKDFLLVIPF 120
                                                                                                                                                                               ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
                                                                                                                                     9
                                                                                                                   1 MAPARSPSPSTQPWEHVNAIQEARRLIANLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
                                                                                            15 MAPARSPSPSTQPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPTCLQTRL
                                                  Gaps
                                                  .
0
88.6%; Score 678; DB 8; Length 128; 100.0%; Pred. No. 2.3e-64; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         DCWEPVQE 142
                                                                                                                                                                                                                                                                                                                DCWEPVOE 128
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AAR79320 standard; protein; 274 AA. (first entry) 25-AUG-1999 AAR79320;

IL-3 containing fusion protein.

interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine; mutant; mutein; fusion protein.

Synthetic.

W09521254-A1

10-AUG-1995.

95WO-US001185. 02-FEB-1995;

94US-00192325 04-FEB-1994;

(SEAR) SEARLE & CO G D.

Easton AM; Caparon MH, Braford-Goldberg SR, Caparon M. Olins PO, Paik K, Thomas JW; Abrams MA, Mckearn JP, Bauer CS, Klein BK,

WPI; 1995-283774/37. N-PSDB; AAQ97183

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An ew fusion protein has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, in which R1 is a mutant or variant of human interleukin-3 (MIL-3) having the present generic sequence, R2 is a second colony stimulating factor (CSF) including cytokine, lymphokine, interleukin, heamatopoietic growth factor or IL-3 variant, and L is a linker. The present sequence corresponds to native hIL-3(1-133) in which 1-14 amino caids cam be deleted from the N-terminal, 1-15 amino acids can be deleted from the N-terminal, 1-15 amino acids can be deleted from the N-terminal, 1-15 amino acids in the region 17-123 are different from those in the native protein. The fusion protein is used to increase heamatopoietic cell production. It is also usedul as an IL-3 antagonist or as a discrete antigenic fragment for production of antibodies useful in immunoassays and immunotherapy.

CC Antagonists are used to block the growth of certain cancer cells and in treatment of asthma. The fusion protein can also be used to stimulate con marrow and blood cell activation and growth in vitro before infusion in the protein has the used synergistic activity and reduced system. The protein has the usual activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects
Fusion proteins comprising a human interleukin-3 variant, a linker a interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
                                                                                                                       Claim 16; Page 87-88; 447pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 274 AA;
   ###X#XDDDDDDDDDDDDDDXX
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207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266 75 ELYKOGLRGSLTKLKGPLTMMASHYKOHCPPTPETSCATOIITFESFKENLKDFLLVIPF 134 74 15 MAPARSPSPSTOPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL Gaps ö Length 274; 0; Indels 88.6%; Score 678; DB 2; L 100.0%; Pred. No. 6.4e-64; iive 0; Mismatches 0; Matches 128; Conservative Query Match Best Local Similarity 셤 g ò

8, 2005, 16:10:22 Search completed: March Job time : 167 secs

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March 8, 2005, 16:13:34 ; Search time 131 Seconds (without alignments) 356.675 Million cell updates/sec
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765
1 MHHHHHHSGIEGRMAPARS.......BNLKDFLLVIPFDCWEPVQE 142
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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GenCore version 5.1.6 • Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1391452 segs, 329044822 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 141, App	Sequence 160, App	Sequence 144, App	Sequence 142, App	Sequence 10, Appl	Sequence 18, Appl	Sequence 1, Appli	Sequence 15, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 15, Appl	Sequence 202, App
	ΔΙ	US-10-083-446-141	US-10-083-446-160	US-10-083-446-144	US-10-083-446-142	US-10-609-346-10	US-09-821-883-18	US-09-800-016-1	US-09-792-793A-15	US-10-400-377-8	US-10-400-708-8	US-10-298-148-8	US-10-375-209A-15	US-10-658-834A-202
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	Query Match Length DB	259	128	274	301	712	127	127	127	127	127	127	127	127
dР	Query	89.2	98.6	88.6	88.6	88.2	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0
	Score	682	678	678	678	675	673	673	673	673	673	673	673	673
	Result No.	1	7	e	4	ហ	9	7	80	σ	10	11	12	13

Sequence 5, Appli Sequence 142, Appl Sequence 114, App Sequence 114, App Sequence 114, App Sequence 115, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 1
6 US-10-743-295-5 6 US-10-773-399-8 5 US-10-773-399-8 6 US-10-743-295-8 1 US-09-923-246-114 4 US-10-295-723-114 4 US-10-295-723-114 4 US-10-295-723-114 4 US-10-295-723-114 5 US-10-131-985-15 5 US-10-116-275-217 5 US-10-116-275-217 5 US-10-116-275-217 5 US-10-116-275-217 6 US-10-411-026-18 6 US-10-410-990-18 6 US-10-410-990-18 6 US-10-410-990-18 6 US-10-410-990-18 6 US-10-410-990-18 6 US-10-410-991-18 6 US-10-449-911A-18 7 US-10-449-911A-18 8 US-10-666-122-5 7 US-10-449-911A-18 8 US-10-668-834A-376 6 US-10-658-834A-376 6 US-10-658-834A-376
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673 673 673 673 673 673 673 673 673 673
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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RESULT 1
US-10-03-46-141
US-10-03-46-141
US-10-03-46-141
US-10-03-46-141
Sequence 141, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
BAUET, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Corperate Patent Dept., Mail Zone 04E
CITY: St. Louis
CUNPUTER READBEE FORM:
MEDIUM TYPE: ISH PC Compatible
COMPUTER READBEE FORM:
MEDIUM TYPE: ISH PC Compatible
COMPUTER: ISH PC
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RESULT 3
US-10-083-446-144
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Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 CLOTRLELYKOGLRGSLTKLKGPLTMMASHYKOHCPPTPETSCATQIITFESFKENLKDF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation Corporate Patent Dept., Mail Zone 04E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

89.2%; Score 682; DB 14; Length 259;
Best Local Similarity 97.0%; Pred. No. 7.2e-64;
Matches 130; Conservative 0; Mismatches 4; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: FOCOMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
                                                                                                                                                         NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 141:
                                                                                                                                                                                                                                            TELEPHONE: (636)737-6257
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
STRANDEDNESS: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 160, Application US/10083446; Publication No. US20030185790A1 GENERAL INFORMATION: APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 800 N. Lindbergh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
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CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
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88.6%; Score 678; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.5e-64;
Matches 128; Conservative 0; Mismatches 0;
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FBB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6452
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-10-083-446-160
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 144, Application US/10083446 Publication No. US20030185790A1 GENERAL INFORMATION:
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CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Abrams, Mark A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
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us-10-723-083-2.rapb

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RESULT 5

US-10-609-346-10

Sequence 10, Application US/10609346

Publication No. US20040063635A1

GENERAL INFORMATION:

APPLICANT: Yu. Zailin

TITLE OF INVENTION: BFFECTS

TITLE OF INVENTION: BFFECTS

FILE REFERENCE: ZYU-0603

CURRENT FILICATION NUMBER: US/10/609,346

CURRENT APPLICATION NUMBER: US 60/392,948

PRIOR PLING DATE: 2002-07-01

SOFTWARE: PatentIn version 3.1

SEQ ID NO 122

LENGTH: 712
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88.6%; Score 678; DB 14; Length 301;
Best Local Similarity 100.0%; Pred. No. 2.3e-63;
Matches 128; Conservative 0; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: G-Feb-2002
CLASSIFICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 19-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 10-JUN-195
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELEPHONE: (656)737-6257
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-083-446-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 301 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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294 DCWEPVQE 301
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TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 MAPARSPSPSTQPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206
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CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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          SOFTWARE: PatentIn Release #1.0, Version #1.25
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Peb-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
PILING DATE: 06-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                               NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 144:
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Publication No. USZ0030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acid
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COMPUTER READABLE FORM
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STATE: Missouri
COUNTRY: USA
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US-10-083-446-142
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Sequence 15, Application US/09792793A

Patent No. US20020168370A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MCDONald, John R.
APPLICANT: COGGINS, PHILIP
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15
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Sequence 8, Application US/10400377

Publication No. US2030162949A1

GENERAL INFORMATION:

APPLICANT: Bolder Biotechnology, Inc.

TITLE OP INVENTION: Derivatives of Growth Hormone and Related Proteins

FILE REFERENCE: 4152-1-PUS

CURRENT APPLICATION NUMBER: US/10/400,377

CURRENT PILING DATE: 2003-03-26

PRIOR PILING DATE: 2000-01-14
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; OTHER INFORMATION: Human Chemokine Polypeptide: GM-CSF
US-09-792-793A-15
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88.0%; Score 673; DB 9; L
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0;
                                                                                               Query Match 88.0%; Score 673; DB 9; I
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0;
                         ORGANISM: Homo sapiens
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ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 CWEPVOE 142
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Patent No. US20020141970A1
GENERAL INPORTATION:
APPLICANT: Pettit, Dean
APPLICANT: Jochheim, Claudia
TITLE OF INVENTION: STABLE AQUEOUS SOLUTIONS OF GRANULOCYTE MACROPHAGE COLONY-STIMU
FILLE REPRENCE: 3253
CURRENT APPLICATION NUMBER: US/09/800,016
CURRENT PILLIOR DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 1
SOPTWARE: PatentIn version 3.0
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                                                                                                                                 75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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                                                                                               15 MAPARSPSPSTOPWEHVNAIQEARRILINISRDTAAEMNETVEVISEMFDLQEPTCLQTRL
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; Sequence 18, Application US/09821883
; Patent No. US20020061310A1
; GENERAL INFORMATION:
   APPLICANT: Laus, Reiner
; APPLICANT: Vidovic, Damir
; APPLICANT: Graddis, Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; TITLE OF INVENTION: Cell-Based Immunotherapy
; TITLE OF INVENTION: 00022.30
; CURRENT FILING DATE: 2001-03-30
; PRIOR PILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; OFTWARE: FRAESE FRAESE (or Windows Version 4.0
Length 712;
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100.0%; Pred. No. 2.5e-63;
iive 0; Mismatches 0;
  88.2%; Score 675; DB 15;
99.2%; Pred. No. 1.5e-62;
tive 1; Mismatches 0;
Query Match
Best Local Similarity 99.2'
Matches 127; Conservative
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Best Local Similarity 100.
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     105 DCWEPVQE 712
                                                                                                                                                                                                                                                                                                      135 DCWEPVOE 142
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US-09-821-883-18
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LENGTH: 127
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LENGTH: 127
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                                                                                                                                                                                                                                                                                                                                                                                                        76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
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Publication No. US20030166865A1

GENERAL INFORMATION:

APPLICANT: Cox III, George N

APPLICANT: Cox III, George N

TITLE OF INVERTION: Derivatives of Growth Hormone and Related Proteins

TITLE OF INVERTION: Derivatives of Growth Hormone and Related Proteins

CURRENT FILIS APPLICATION NUMBER: US/10/400, 708

CURRENT FILING DATE: 2003-03-26

PRIOR PELING DATE: 2000-01-14

PRIOR PLING DATE: 2000-01-14

PRIOR PLING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTIN VET: 2.0
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88.0%; Score 673; DB 14; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                        , ORGANISM: Homo sapiens
US-10-400-377-8
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; ORGANISM: Homo sapiens
US-10-400-708-8
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                                                                                                                                        TYPE: PRT
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Sequence 8, Application US/10298148 Publication No. US20030171284A1 GENERAL INFORMATION: APPLICANT: COX III, George N

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Sequence 15, Application US/10375209A

Publication No. US20030215421A1

Publication No. US20030215421A1

GENERAL INFORMATION:

APPLICANT: McDonald, John R.

APPLICANT: Cogajins, Philip

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REPREBENCE: 25020-601E

CURRENT APPLICATION NUMBER: US/10/375,209A

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

LENGTH: 127
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APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REPERENCE: 415.2-1.FUS
CURRENT APPLICATION NUMBER: US/10/298,148
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR PILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 127
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US-10-375-209A-15
                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-8
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ORGANISM: homo sapien
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Gaps

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0; Indels

Length 127;

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Sequence 8, Application US/10773939

Fublication No. US20040175356A1

GENERAL INFORMATION:

APPLICANT: CAN III, George N

TITLE OF INVENTION:

FILE REFERENCE: 4152-1-P05

CURRENT APPLICATION NUMBER: US/10/773,939

CURRENT FILING DATE: 2004-02-05

FRIOR APPLICATION NUMBER: US/09/462,941

FRIOR PILING DATE: 2003-03-26

PRIOR FILING DATE: 2003-03-26

FRIOR FILING DATE: 2000-03-26

FRIOR FILING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 8

LEASTH 127

LENGTH: 127

LENGTH: 127
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                                      Query Match

88.0%; Score 673; DB 16;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0;
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US-10-773-939-8
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Job time : 132 secs
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US-10-773-939-8
US-10-743-295-5
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                                 Sequence 2024. Application US/10658834A

Sequence 2025. Application US/10658834A

Publication No. US20040132977A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Rene

APPLICANT: Origa, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.

TITLE OF INVENTION: Molecules and Related Applications

FILE REFERENCE: 38751-92.

FILE REFERENCE: 38751-92.

CURRENT APPLICATION NUMBER: US/10/658,834A

CURRENT FILING DATE: 2003-09-08

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR PLING DATE: 2002-09-09

PRIOR PILING DATE: 2002-09-09

PRIOR PILING DATE: 2002-09-09

PRIOR PILING DATE: 2002-09-09
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APPLICANT: Sherman, Merry R.
APPLICANT: Saifer, Mark G.P.
APPLICANT: Saifer, Mark G.P.
APPLICANT: Saifer, Mark G.P.
APPLICANT: Saifer, David
TITLE OF INVENTION: POLYMER CONJUGATES OF CYTOKINES, CHEMOKINES, GROWTH FACTORS, POLY
TITLE OF INVENTION: HORMONES AND ANTAGONISTS THEREOF WITH PRESERVED RECEPTOR-BINDING
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 2057.0060002/JAG/BJD
CURRENT APPLICATION NUMBER: 60/479,914
PRIOR APPLICATION NUMBER: 60/479,914
PRIOR FILING DATE: 2003-12-23
PRIOR FILING DATE: 2003-12-26
PRIOR FILING DATE: 2003-12-26
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88.0%; Score 673; DB 16;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0;
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DATABASE ENTRY DATE: 1996-05-02
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 127
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SOFWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 202
LENGTH: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                    Gaps
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  Length 127;
                                                    Indels
Query Match 88.0%; Score 673; DB 16; Best Local Similarity 100.0%; Pred. No. 2.5e-63; Matches 127; Conservative 0; Mismatches 0;
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RESULT 2
US-08-468-609A-141
; Sequence 141, Application US/08468609A
                               MOLECULE TYPE: protein US-08-469-318-141
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Sequence 141, App
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Sequence 160, App
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Sequence 160, App
Sequence 160, App
Sequence 144, App
Sequence 142, App
Sequence 143, App
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                                                                          March 8, 2005, 16:05:14 ; Search time 42 Seconds
(without alignments)
252.385 Million cell updates/sec
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1 MHHHHHHSGIEGRWAPARS......BNLKDFLLVIPFDCWEPVQE
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    /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-468-609A-141
US-08-762-227A-141
US-08-60-318-141
US-08-69-318-160
US-08-468-609A-160
US-08-468-609A-160
US-08-762-227A-160
US-08-762-227A-144
US-08-762-227A-142
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US-09-462-941-8
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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Maximum DB
                                                                                                                                                                                                     Searched:
                                                                                                                                                Sequence:
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Sequence 114, App
Sequence 11, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
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Protein
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Pred. No. 1e-69;
0; Mismatches 4; Indel8
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Fatent No. 602253
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPC
TATLE OF INVENTION NUMBER: US/08/469,318
FILING DATE:
PRIOR APPLICATION NUMBER: 08/446,872
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/446,872
                                 US-08-318-193-8
US-08-318-193-10
US-09-146-283-2
US-09-344-195-2
US-09-344-195-2
US-09-344-195-2
US-09-344-195-4
                    r-US95-08950-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.2%;
Best Local Similarity 97.0%;
Matches 130; Conservative (
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69 CLQTRLBLYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
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                                                                                                                                                                                   TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS: 187
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-UN-1995
                                                                                                                                                                                                                                                                             Dennis A. Bennett, G.D. Searle & Co. Corporate Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
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Pred. No. 1e-69;
0; Mismatches
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US-08-762-227A-141
'S Sequence 141, Application US/08762227A
'; Patent No. 6436387
'; Patent No. 6436387
'; APPLICANT: Abrams, Mark A.
'; APPLICANT: Bauer, S. C.
'; Braford-Goldberg, Sarah R.
       Sarah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Braford-Goldberg,
Caparon, Maire H.
Easton, Alan M.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 141: SEQUENCE CHARACTERISTICS:
                                                                       Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.0%;
Matches 130; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,
                                                                                                                                                                Thomas, John W.
                                                                                                                                                                                                                                                                                                                                P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (314) 737-6972
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                        60680
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                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                           APPLICANT: Thomas, John W. TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRILINLSRDTAAEMNETVEVISEMFDLQEPT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRIINLSRDTAAEMNETVEVISEMFDLQEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.2%; Score 682; DB 3; Length 259; 97.0%; Pred. No. 1e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-UNN-1995
CLLASIFFICATION:
PRICE TION: PRICE 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENDECT, Deimis A.
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION NUMBER: C-2790/3
TELECOMMUNICATION NUMBER: C-2790/3
TELECOMMUNICATION NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      3: Dennis A. Bennett, G.D. Searle & Co.,
3: Corporate Patent Dept.
P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                     Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-446-872A-141
; Sequence 141, Application US/08446872A
; Patent No. 636.1977
; Patent Linforkhalion:
days Applicant: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 LLVIPFDCWEPVOE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 259 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.09
Matches 130; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              Chicago
: Illinois
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60680
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                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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STREET: P.
                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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186 CLQTRLELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

88.6%; Score 678; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 128; Conservative 0; Mismatches 0; Indels
                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01185

FILING DATE: 02-FEB-1995

CLASSIFICATION:

PRICH APPLICATION:

PRICH APPLICATION:

PRICH APPLICATION:

PRICH APPLICATION:

APPLICATION NUMBER: US 08/192325

FILING DATE: 14-FEB-1994

INFORMATION FOR SEQ ID NO: 141:

SEQUENCE CHARACTERISTICS:

LENGTH: 259 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,318
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 682; DB 5;
Pred. No. 1e-69;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 160, Application US/08469318 Patent No. 6022535
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 LLVIPFDCWEPVQE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.0
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein PCT-US95-01185-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 CLQTRLELYKQGLRGSLTKLKGPLTWMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 CLOTRLELYKOGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRIINLSRDTAAEMNETVEVISEMFDLQEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 89.2%; Score 682; DB 4; Length 259; Best Local Similarity 97.0%; Pred. No. 1e-69; Matches 130; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.I
Corporate Patent Dept
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: «Unknown»

TOPOLGGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-08-762-227A-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-279
TELECOMMUNICATION INPORMATION:
TELEPHONE: (708)470-6501
TELEPHONE: (708)470-6681
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        Fusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 141, Application PC/TUS9501185
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-
TITLE OF INVENTION: Protein
Baston, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 259 amino acids TYPE: amino acid
                                                                                                           Thomas, John W.
                                                                                                                                                                          NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 LLVIPFDCWEPVOE 142
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                                                                                                                                                                                                                                                                                                                                                  ZIP: 60680
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-01185-141
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75 BLYKOGLRGSLIKLKGPLIMMASHYKQHCPPIPETSCATQIITFBSFKENLKDFLLVIPF 134
                                        61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION UMBER: US 08/192,325
FILING APPLICATION TATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis TITLE OF INVENTION: Fusion Protein NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS: ADDRESSE: Dennis A. Bennett, G.D. Searle & Co., ADDRESSE: Corporate Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Dennis A. Bennett, G.D. Searle & Co., E: Corporate Patent Dept.
P. O. Box 5110
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Pred. No. 1.1e-69;
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88.6%; Score 678; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 128; Conservative 0; Mismatches
                                                                                                                                                                                                                     Sequence 160, Application US/08446872A
Patent No. 6361977
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,547 REFERENCE/DOCKET NUMBER: C-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Palk, Kumnan
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Braford-Goldberg,
Caparon, Maire H.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-446-872A-160
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                                                                                           135 DCWEPVQE 142
                                                                                                                            121 DCWEPVQE 128
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STATE: Illinois
COUNTRY: USA
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APPLICANT:
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IITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
                                                                                             61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120
                                                                       75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
                         1 MAPARSPSPSTQPWEHVNAIQEARRILINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60
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15 MAPARSPSPSTQPWEHVNAIQEARRLINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Dennis A. Bennett, G.D. Searle & Co., B: Corporate Patent Dept.
P. O. Box 5110
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Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
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INFORMATION FOR SEQ ID NO: 160: SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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ADDRESSEE: Dennis A.
                                                                                                                                             135 DCWEPVQE 142
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Best Local Similarity
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STATE: Illinois
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US-08-468-609A-160
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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61 ELYKOGLEGSLITKLKGPLITMASHYKOHCPPTPETSCATOIIITFESFKENLKDFLLLVIPF 120
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         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        Multivariant IL-3 Hematopoiesis Fusion
Protein
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 196

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Relase #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 02-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 160:
SUGUENCE GIRARACTERISTICS:
FELING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 160:
SUGUENCE GIRARACTERISTICS:
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100.0%; Pred. No. 1.1e-69;
ive 0; Mismatches 0;
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; Sequence 160, Application PC/TUS9501185
; GENERAL INFORMATION:
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TYPE: amino acid
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Best Local Similarity 100.0°
Matches 128; Conservative
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PCT-US95-01185-160
                                                                                            135 DCWEPVQE 142
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CLASSIFICATION:
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61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 12.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas, John W. TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEFRAM: (708)470-6801
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
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; SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-08-762-227A-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion Protein
                                                                                                                                                                                                                        Sequence 160, Application US/08762227A
Patent No. 6436387
GENERAL INFORMATION:
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Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 128; Conservative
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                     135 DCWEPVQE 142
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                                                                                                                                                                                                                                                                                                       15 MAPARSPSPSTOPWEHVWAIQEARRLINLSRDTAAEMWETVEVISEMFDLQEPTCLQTRL
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN 1995
CLASSIFICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN 1995
ATTON NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTONNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,577
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APPLICANT: Palk, Kunnan
APPLICANT: Palk, Kunnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
STRIET: P. O. STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                     Pred. No. 3.2e-69;
                                                                                                                                                                                                          88.6%; Score 678; DB 3;
100.0%; Pred. No. 3.2e-69
tive 0; Mismatches 0
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Braford-Goldberg, Sarah
Caparon, Maire H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 144, Application US/08446872A Patent No. 6361977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Tr. Klein, Barbara K.
Tr. McKearn, John P.
Tr. Olins, Peter O.
Tr. Paik, Kumnan
    144:
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TELEPAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Abrams, Mark A.
                                                : 274 amino acids amino acid
                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 128; Conservative
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                      , MOLECULE TYPE: protein US-08-468-609A-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                       linear
                                                                                            STRANDEDNESS
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                                                                                                                       TOPOLOGY:
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APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: McKearn, John P.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
WUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 ELYKQGLRGSLTKLKGPITWMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266
                                                                                                                                                                                                                                                                                                                                                                                                             75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITPESFKENLKDFLLVIPF 134
                                                                                                                                                                                                                                                                                                                                                                                     15 MAPARSPSPSTOPWEHVNAIQEARRILINLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL
                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                   Query Match 88.6%; Score 678; DB 3; Length 274; Best Local Similarity 100.0%; Pred. No. 3.2e-69; Matches 128; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 08/192,325
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abrams, Mark A.
Bauer, S. C.
Bradford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
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CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 144, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
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                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-318-144
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US-08-468-609A-144
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APPLICANT:
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Search completed: March 8, 2005, 16:14:58
Job time : 43 secs
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                                                                                                                                                                                                      15 MAPARSPSPSTOPWEHVNAIOEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL
                                                                                                                                                                    Gaps
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                                                                                                                             Length 274;
                                                                                                                                                                  0, Indels
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ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
                                                                                                                            88.6%; Score 678; DB 3; I
100.0%; Pred. No. 3.2e-69;
tive 0; Mismatches 0;
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APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braford-Goldberg, Sarah R. Caparon, Maire H. Easton, Alan M. Klein, Barbara K. McKearn, John P. Olins, Peter O. Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 144, Application US/08762227A
Patent No. 6436387
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (708)470-6881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abrams, Mark A. Bauer, S. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 144
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274 amino acids
                                                                                                                             Query Match
Best Local Similarity 100.
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
                                                                      ; MOLECULE TYPE: protein US-08-446-872A-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                          DCWEPVOE 142
                   TYPE: amino acid STRANDEDNESS:
                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-762-227A-144
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207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266
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                                                                                                                                                                                                                                                                                                                                                             147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206
                                                                                                                                                                                                                                                                                                                                                                                                                   75 ELYKOGLRGSLTKLKGPLTMMASHYKOHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                 Length 274;
                                                                                                                                                                                                                                                 Indels
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APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 02-FEB-1995
                                                                                                                                                                                           Query Match 88.6%; Score 678; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.2e-69;
Matches 128; Conservative 0; Mismatches 0;
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88.6%; Score 678; DB 5; Best Local Similarity 100.0%; Pred. No. 3.2e-69; Matches 128; Conservative 0; Mismatches 0;
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-08-762-227A-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 144, Application PC/TUS9501185
GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 196
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-FEB-1995
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/19
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 144:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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bioactive human
factor (GM-CSF) and other
AR202217 Sequence
AR22319 Sequence
A00368 Artificial
A00368 Artificial
A14305 GM-CSF gene
CQ721607 Sequence
CQ803372 Sequence
E0229 DNA encodin
108093 Sequence 1
108091 Sequence 1
108091 Sequence 1
108094 Sequence 1
10810 Sequence 1
10910 Sequence 1
10916 Sequence 2
M11220 Human granu
AR082744 Sequence
AR09963 Sequence
AR14394 Sequence
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AR147690 Sequence
AR36478 Sequence
AR36478 Sequence
AR36445 Sequence
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AR36478 Sequence
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AR36478 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct
synthetic construct
other sequences; artificial sequences.
I (bases I to 905)
An expression system for the secretion of bic granulocyte macrophage colony stimulating factive in Ep 0352707-A 21 31-JAN-1990;
Cangene Corporation
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 A20088 905 bp DNA BamHI-HindIII fragment in vector pAEO.GMCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;

    .905
    dorganism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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86.9%; Pred. No. 3.6e-38;
iive 0; Mismatches 53
                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                      HUMGMCSFA
AR082744
                               A00368
A14305
A14306
CQ721607
CQ803372
E02287
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AR533388
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[08094
[0840]
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Best Local Similarity 86.9
Matches 351; Conservative
  502
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ACCESSION
VERSION
KEYWORDS
SOURCE
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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PstI-Hind I
PstI-Hind I
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A20083 Pet1-Hind I
A20086 BamH1-HindI
A20087 BamH1-HindI
A20087 BamH1-HindI
A20087 Sequence
149838 Sequence
CQ834915 Sequence
AR202206 Sequence
AR202206 Sequence
AR202206 Sequence
AR202206 Sequence
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                                                                        March 11, 2005, 10:03:16; Search time 2574 Seconds (without alignments) 8621.791 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR363245 Sequence
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                      nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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AR223282 Sequence AR202220 Sequence AR223222 Sequence

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Garvin, R.T. and Malek, L.T.
Expression system for the secretion of bioactive human granulocyte
macrophage colony stimulating factor (GM-CSF) and other
heterologous proteins from streptomyces
Patent: US 5200327-A 3 06-APR-1993;
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.larity 86.9%; Pred. No. 3.6e-38;
Conservative 0; Mismatches 53; Indels 0.
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Sequence 3 from patent US 5200327.
AR363245

    905
    /organism="unknown"
    /mol_type="genomic DNA"

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other sequences; artificial sequences.

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( based 1.0 966)

Garvin,R.T. and Malek,L.T.

An expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomyces heterologous proteins from streptomyces Patent: EP 0352707-A 22 31-JAN-1990; Cangene Corporation

Location/Qualifiers
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Garvin,R.T. and Malek,L.T.
Garvin,R.T. and Malek,L.T.
Bxpression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from steptomyces
heterologous proteins from steptomyces
Patent: US 5641663-A 9 24-UM-1997;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                    /organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                           69.7%; Score 319.2; DB 6
86.9%; Pred. No. 3.6e-38;
iive 0; Mismatches 53
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/organism="unknown"

PAT 18-AUG-1994

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PAT 18-AUG-1994
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                                                                                                                   240
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268 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 CTGTACAAGGGGCTCCGGGGCAGCCTCACCAAGGTCAAGGGGCCGCTGACCATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 GCGTCCCACTACAAACAGCACTGCCCCCCCAACGGAGAGGTCGTGGGGCGCACCAAATC
                                                                                                                        181 CTGTACAAGCAGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG
                                                                                                                                                                      GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCCAGATC
                                                                                                                                                                                                                241 GCGTCCCACTACAAACAGCACTGCCCCCCACGCCGGAGACGTCGTGCGCCACAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCTTCGAC
                                                                                                                                                                                                                                                               ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other sequences; artificial sequences.

1 (bases 1 to 322)

Garvin,R.T. and Malek,L.T.
An expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and heterologous proteins from streptomyces Patent: EP 0352707-41 31-JAN-1990;

Cangene Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.5%; Score 318.4; DB 6; 89.3%; Pred. No. 5.6e-38;
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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GM-CSF.
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PstI-Hind III fragment encoding
A20083
                                                                                                                                                                                                                                                                                                                                                                                       361 TGCTGGGAGCCGGTGCAGGAGTGA 384
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Best Local Similarity 89.3
Matches 343; Conservative
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1 (Dases 1 to 384)
Garvin,R.T. and Malek,L.T.
Garvin,R.T. and Malek,L.T.
Granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomyces
Patent: EP 0352707-A 13 31-GAN-1990;
Cangene Corporation
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                                                                                                                                                                                                                561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      741
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                                                                                                                                                                                                                                                                                                                                                                                     CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT
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89.3%; Pred. No. 5.7e-38;
iive 0; Mismatches 41;
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                                                                    Score 319.2; DB 6,
Pred. No. 3.6e-38;
0; Mismatches 53
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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PstI-Hind III fragment encoding GM-CSF.
A20082
  DNA"
  /mol_type="unassigned
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                                                                    tch 69.7%; sal Similarity 86.9%; 351; Conservative
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synthetic construct
synthetic construct
other sequences, artificial sequences.
( lassel to 986)
Garvin,R.T. and Malek,L.T.
An expression system for the secretion of bioactive human
granulocyte macrophage colony stimulating factor (GM-CSF) and other
heterologous proteins from streptomyces
Patent: EP 0352707-A 20 31-JAN-1990;
Cangene Corporation
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                                                                                                                                                                                       69.5%; Score 318.4; DB 6
89.3%; Pred. No. 4.7e-38;
ive 0; Mismatches 41

    .896
    ^organisa="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

 heterologous proteins from streptomyces
Patent: BP 0352707-A 19 31-JAN-1990;
Cangene Corporation
Location/Qualifiers

    .896
    /organism="synthetic const./mol_type="unassigned DNA"/db_xref="taxon:32630"

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A20087.1 GI:578984
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Best Local Similarity 89.3
Matches 343; Conservative
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1 (bases 1 to 896)
Garvin,R.T. and Malek,L.T.
An expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other
                                                                                                                 PAT 07-0CT-1997
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Garvin,R.T. and Malek,L.T.
Expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from steptomyces
Patent: US 5641663-A 1 24-JUN-1997;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174
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BamHI-HindIII fragment in vector pAPO.GMCSF.
A20086.1 GI:583267
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Pred. No. 5.6e-38;
0; Mismatches 41,
                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                             392 bp Sequence 1 from patent US 5641663.
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Matches 343; Conservative
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TGCTGGGAGCCGGTGCAGGAGT 436
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           1 (bases 1 to 386)
Garvin, K.T. and Malek, L.T.
Expression system for the secretion of bioactive human granulocyte
macrophage colony stimulating factor (GM-CSF) and other
heterologous proteins from streptomyces
hatch: US 5200327-A 10-APR-1993;
Location/Qualifiers
                                                                                                                                                                                                                                                                               136 CTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTC 195
                                                                                                                                                                                                                                                                                                CTCTCGCGGGACACGCCGCCGGGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTC 143
                                                                                                                                                                                                                                                                                                                                    GATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGC 255
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Method and device for optimizing a nucleotide sequence for purpose of expression of a protein
Patent: WO 2004059556-A 2 15-JUL-2004;
Geneart GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                    Score 315; DB 6; Length 386;
Pred. No. 1.8e-37;
0; Mismatches 30; Indels
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84.0%; Pred. No. 6.1e-33;
ive 0; Mismatches 61;
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Sequence 2 from Patent WO2004059556.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                 /organism="unknown"
/mol_type="genomic DNA"
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91.7%;
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                                                                                                                                                                      Query Match
Best Local Similarity 91.7
Matches 333; Conservative
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PAT 20-APR-2002 ö 213 615 Dauer, S. Christopher., Abrams, M. Allen., Braford-Goldberg, S. Ruth., Caparon, M. Helena., Easton, A. Michael., Klein, B. Kure., McKearn, J. P., Olins, P.O., Paik, K. and Thomas, J. W. Methods of using multivariant IL-3 hematopoiesis fusion protein Patent: US 6361977-A 55 26-MAR-2002; 435 495 555 273 114 174 171 231 294 291 354 351 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414 411 94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGGCGACACGCC 153 274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333 GCCCTGCCAGAAGCCCTAGCCCTAGCACACAGCCTTGGGAGCACGTGAATGCCATCCAG 111 93 112 GAGGCCAGGAGACTGCTGAACCTGAGCAGATACAGCCGCCGAGATGAACGAGACGTG GAGGTGATCAGCGAGATGTTCGACCTGCAGGAGCCTACATGCCTGCAGACCCGGCTGGAG 292 GCCAGCCACTACAAGCAGCACTGCCCTCCTACCCTGAGACAAGCTGCGCCACCCAGATC ATCACCTTCGAGAGCTTCAAGGAGAAACCTGAAGGACTTCCTGCTGGTGGTCCCCTTCGAT GCCGAGATGAACGAGACGTGAGCTGATCTCCGAGATGTTCGATCTCCCAGGAGCCGACC gergagargaargaagragaagrgararcagaaargrrrgacerceagagecgaer 556 receracadacececercadecreracadecadecerecegededecreadecre GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACGCCGCCGAGATGAACGAGACCGTG GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 34 TCCGGCATCGAGGCCGCATGGCGCCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 376 TCTGGCGGCGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG CTGTACAAGCAGGCCTCCGCGCAGCCTCACCAAGCTCAAGGCCCGCTCACCATGATG TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC Gaps ; 0 Length 777; linear Indels Score 283.6; DB 6; Pred. No. 7.1e-33; Query Match 61.9%; Score 283.6; Best Local Similarity 81.6%; Pred. No. 7.1e Matches 328; Conservative 0; Mismatches AR202206 777 bp Sequence 55 from patent US 6361977. /mol_type="unassigned DNA"

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PAT 26-SEP-2002
334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAAACCTCAAGGACTTC 393
                                                                                       214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGCCTCCGCGGCAGCCTCACCAAGCTC 273
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Unclassified.
1 (bases 1 to 777)
Bauer, S.C., Abrams, M.A., Braford-Goldberg, S.R., Caparon, M.H.,
Baston, A.M., Klein, B.K., McKearn, J.P., Olins, P.O., Palk, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 TCCGGCATCGAGGCCGCATGGCGCCAGCGCGCGGGCCCGAGCCCGTCCAGCCGTGG
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Methods of ex-vivo expansion of hematopoietic cells using multivariant IL-3 hematopoieeis chimera proteins

Patent: US 6436387-A 55 20-AUG-2002;

Location/Qualifiers
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Sequence 55 from patent US 6436387.
AR223208
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/mol_type="genomic DNA"
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Search completed: March 11, 2005, 16:42:03 Job time : 2582 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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using sw model nucleic search, nucleic ĕ March 11, 2005, 15:26:31; Search time 145 Seconds (without alignments) 5168.377 Million cell updates/sec Run on:

US-10-723-083-1 Title: Perfect score:

1 cggcccgggatgcaccacca.....gctagcgtcgacgcatgccg 458 Sequence:

Gapext 1.0 IDENTITY NUC Gapop 10.0 , Scoring table:

1202784 segs, 818138359 residues Searched:

Total number of hits satisfying chosen parameters:

2405568

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Database

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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* Patents NA:* 2 W 4 W 0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
1	319.2	69.7	1	9	5200327-3	Patent No. 5200327	
7	319.2	69.7			5200327-3	Patent No. 5200327	
٣	319.2	69.7			US-08-318-193-9		
4	318.4	69.5			US-08-318-193-1		
Ŋ	318.4	69.5			5200327-2	Patent No. 5200327	
9	318.4	69.5	968	9	5200327-2	8	
7	318.4	69.5			US-08-318-193-7	g	
œ	315	68.8			5200327-1	Patent No. 5200327	
6	315	68.8			5200327-1	Patent No. 5200327	
10	312.6	68.3	435	-	US-10-188-056-31	Sequence 31, Appl	
11	311	67.9		-	US-10-188-056-33	33,	
12	283.6	61.9		n	US-08-469-318-55	Sequence 55, Appl	
13	283.6	61.9	777	m	US-08-468-609A-55	55,	
14	283.6	61.9		ო	US-08-446-872A-55	55,	
15	283.6		777	m	US-08-762-227A-55	55,	
16	283.6			ß	PCT-US95-01185-55	55,	
17	283			ო	US-08-469-318-176	176,	
18	283	61.8	402	٣	US-08-468-609A-176	176,	
19	283	61.8		ო	US-08-446-872A-176	176,	
20	283	61.8	402	m	US-08-762-227A-176	176,	
21	283	61.8			PCT-US95-01185-176	176,	
22	281	61.4			US-08-469-318-69	69	
23	281	61.4		m	US-08-468-609A-69	69	
24	281	61.4		٣	US-08-446-872A-69	Sequence 69, Appl	
25	281	61.4	82		US-08-762-227A-69	69	
56	281	61.4	822	ហ	PCT-US95-01185-69	9	
27	281	61.4	903	m	US-08-469-318-66	Sequence 66, Appl	

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RESULT

Sequence 66, Appl Sequence 66, Appl	Sequence 66, Appl Sequence 66, Appl	Sequence 3, Appli Sequence 3, Appli	Sequence 3, Appli Patent No. 5391485	Patent No. 5391485	Patent No. 5229496	Patent No. 5229496	Sequence 275, App	Sequence 8, Appli	Sequence 8, Appli	Sequence 1195, Ap	Sequence 3, Appli	Sequence 12, Appl	Sequence 1, Appli
US-08-468-609A-66 US-08-446-872A-66	US-08-762-227A-66 PCT-US95-01185-66	US-09-146-283-3 US-08-579-823A-3	US-09-344-195-3 5391485-2	5391485-2	5229496-1	5229496-1	US-09-976-594-275	US-08-848-760B-8	US-09-826-025-8	US-09-016-434-1195	US-09-310-842-3	US-08-750-128-12	US-09-146-283-1
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ALIGNMENTS

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802 CGTCGTGCGCCACCCCAGATCATCACGTTCGAGTCGTTCAAGGAGAAACCTGAAGGACTTCC 861
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                                         APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
BIOACTUVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
FFACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
STREPTOMYCES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/07/224,568
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Pred. No. 1e-60;
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Best Local Similarity 86.9%;
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                          5200327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACACCGCCG 154
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Retent No. 5641663
Retent No. 5641
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                                                                                        APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION; BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING; FRACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.7%; Score 319.2; DB 86.9%; Pred. No. 1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/224,568
FILING DATE: 26-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foley & Lardner
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Matches 351; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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: USA
                                                    Patent No. 5200327
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LENGTH: 905
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US-08-318-193-9
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APPLICANT: GARVIN, ROBERT T.

APPLICANT: GARVIN, ROBERT T.

APPLICANT: MALEK, Lawrence T.

TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

NUMBER OF SEQUENCES: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 CCGCCTCCGGGGCGTCTGCAGCCCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Other nucleic acid; DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.7%; Score 319.2; DB
86.9%; Pred. No. 1e-60;
tive 0; Mismatches
                                                                                                                                                                                           ATTORREY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
US/08/318,193
                                                                                                                                                                   US 07/224,568
                                                                                                                 US/07/935,314
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Patent No. 5641663
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 86.9
Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
APPLICATION NUMBER: 1
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55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
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                                    RESULT 5
5200327
7 PARENT NO. 5200327
7 TI JOHN THE SECRET T., MALEK, LAWRENCE T.
7 TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF 1910ACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING FROM (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T.

TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION C; BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING ; FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM STREPTOMYCES

NUMBER OF SEQUENCES: 24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/224,568

FILING DATE: 26-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IndelB
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Pred. No. 1.5e-60;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
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Pred. No. 1.5e-60;
0; Mismatches 41
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APPLICATION NUMBER: US/07/224,568
FILING DATE: 26-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.5%;
89.3%;
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Best Local Similarity 89.3%;
Matches 343; Conservative
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Best Local Similarity 89.3
Matches 343; Conservative
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Indels
                                                                                                                                                                                                                                                                              JULIARY SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/318,193
FILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,314
FILING DATE: APPLICATION DATA: APPLICATION NUMBER: US/07/935,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/224,568
ATTONEX/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/POCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:
                                                           1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGGGAGCCGGTGCAGGAGTGA 438
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                                                                                                                                                                              ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703)683-4109
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 343; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
                                                                                               Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5..385
                                                                                                                                Virginia
                                                                                                                      STATE: Virgin
                                ADDRESSEE:
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DESCRIPTION: Synthetic DNA oligonucleotide
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                 FEATURE:
NAME/KEY:
LOCATION:
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US-08-318-193-7
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;Patent No.
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                                     175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
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                  GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACACCGCCGCCGAGATGAACGAGACCGTG 174
                                                                                                                                                 CTGTACAAGCAGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG: 294
                                                                                                                                                                                  ATCACCTTCGAGAGACCTTCAAGGAGAACCTCCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: GRAVIN, Robert T.

APPLICANT: MALEK, Lawrence T.

TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                        633 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: STREET: STREET: STREET: STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                  415 TGCTGGGAGCCGGTGCAGGAGTGA 438
                                                                                                                                                                                                                                                                                                                                                                    873 TGCTGGGAGCCGGTGCAGGAGTGA 896
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FILING DATE:
FLISSIFICATION: 435
FILING PAPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08318193
Patent No. 5641663
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(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-318-193-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 CTCTCCCGCGACACCCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTC
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                                                                                    Length 900;
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TITLE OF INVENTION: EXPERSION SYSTEM FOR THE SECRETION
BLOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY SIMULATING
FROTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                      69.5%; Score 318.4; DB 1;
89.3%; Pred. No. 1.6e-60;
iive 0; Mismatches 41;
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Pred. No. 7.5e-60;
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NUMBER OF SEQUENCES: 24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/224,568

FILING DATE: 26-JUL-1988
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Best Local Similarity 91.7%;
Matches 333; Conservative
                                                                                        Query Match 69.5
Best Local Similarity 89.3
Matches 343; Conservative
CDS
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Sequence 33, Application US/10188056 Patent No. 6809191 GENERAL INFORMATION:
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                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                76 CCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAAC 135
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GGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCAC 263
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Pred. No. 7.5e-60;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                    $200327-1
;Patent No. $200327
APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/224,568
FILLING DATE: 26-JUL-1988
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US-10-188-056-31
Sequence 31, Application US/10188056
Patent No. 6809191
GENERAL INFORMATION:
APPLICANT: Qiu, Jian-Tai,
APPLICANT: Lai, Wan-Ching
APPLICANT: Clu, Yong Liang
APPLICANT: Li, Frank Q.
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Best Local Similarity 91.7%;
Matches 333; Conservative
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TGA 386
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APPLICANT: Olu, Man-Ching
APPLICANT: Lai, Wan-Ching
APPLICANT: Lai, Wan-Ching
APPLICANT: Li, Frank O.
TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
FILE REFERENCE: 3781-004-27
CURRENT PILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 435
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TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences FILE REFERENCE: 3781-004-27
CURRENT APPLICATION NUMBER: US/10/188,056
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 435
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Pred. No. 5.7e-59;
0; Mismatches 75,
                                                                                                                                                                                                                                                                                                            Query Match
68.3%; Score 312.6; DB 4
Best Local Similarity 82.8%; Pred. No. 2.6e-59;
Matches 357; Conservative 0; Mismatches 74
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Best Local Similarity 82.6%;
Matches 356; Conservative
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APPLICANT: Thomas, John W. TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            676 ACTTCCTGTGCCAACCCAGATTATCACCTTTGAAAGTTTTCAAAGAGAACCTGAAGGACTTC 735
GCCGAGATGAACGAGACCGTGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC
                                                                                                                                                                               496 GCTGAGATGAATGAAACAGTAGAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                   274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCGGAG
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CURRENT APPLICATION DATA:
ELLOATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
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APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sarah
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STORTWARE: Patentin Release #1.0.
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Patent No. 6030812
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Bauer, S. C.
Braford-Goldberg, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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Easton, Alan M.
Klein, Barbara K.
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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ADDRESSEE:
STREET: P.
CITY: Chica
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Protein
196
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TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
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Pred. No. 5.8e-53;
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Patent No. 6022535
GENERAL INFORMATION:
APPLICANT:
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APPLICATION NUMBER: 08/446,872
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ilarity 81.6%;
Conservative
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
Matches 328; Conserv
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US-08-469-318-55
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APPLICATION NUMBER:
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                                                                       Length 777;
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APPLICANT ADrams, Mark A.
APPLICANT Bauer, S. C.
APPLICANT Bater, S. C.
APPLICANT Caparon, Maire H.
APPLICANT: Ration, Maire H.
APPLICANT: Klein, Barbara K.
APPLICANT: McRearn, John P.
APPLICANT: Paik, Kunnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Pusion Protein
                                                                                                          74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., ADDRESSEE: Corporate Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                         DB 3;
                                                                      61.9%; Score 283.6; DB 3
81.6%; Pred. No. 5.8e-53;
live 0; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-446-872A-55
; Sequence 55, Application US/08446872A
; rent No. 6361977
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-609A-55
                                                                                  Best Local Similarity 81.6
Matches 328; Conservative
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ADDRESSEE: Dennis A.
ADDRESSEE: Corporate
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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: Illinois
RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334
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                                                                       Query Match
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ADDRESSEB: Dennis A. Bennett, G.D. Searle & Co. Corporate Patent Dept.
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 203.6; DB 3;
Pred. No. 5.8e-53;
0; Mismatches 74;
                                                             NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314,737-696
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
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US 08/192,325
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Bauer, S. C.
Bradford-Goldberg, St.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas, John W.
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
61.9%;
Best Local Similarity 81.6%;
Matches 328; Conservative
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                   FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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616 Addescecerreaceareareaceaeceaeceaecaecaecaecaecereceaececeeaa 675
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                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: (708)470-6881
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
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Best Local Similarity 81.6
Matches 328; Conservative
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Search completed: March 11, 2005, 17:26:43 Job time : 148 secs

C 25 166 36.2 531 4 BG2. 26 139 30.3 274 1 AA3. C 27 124 27.1 244 4 BG2. 28 119.2 26.0 647 4 BG2. C 29 114.4 25.0 517 6 CB4. 30 104.8 22.9 269 7 CF3. 31 103.6 22.4 483 1 AIII	88.8 19.4 470 1 69 15.1 892 9 67 14.6 138 2 63.8 13.9 697 9 59.8 13.1 457 5 59 12.9 160 7 58.2 12.7 830 9	42 58 12.7 136 7 43 57.8 12.6 881 9 44 57 12.4 747 9 45 56.8 12.4 671 6	T 1	LOCUS MA207707 DEFINITION UI-H-BIZ-age-e-09-0-UI.8. MAGE:2724184 3', mRNA 86 ACCESSION AW207707 VERSION AW207707 VERSION AW207707.1 GI:6507203 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens EUKAATYOCA; Metazoa; Chorr MAMMALIA; EUKAATYOCA; Metazoa; EUKAATYOCA; Metazoa; Chorr MAMMALIA; EUKAATYOCA; Metazoa; EUKAATYOCA; Metazoa;		INTOTATION TO THE PETUDING WWW-bio.llnl.gov/bbrp/im Seq primer: M13 Forward Seq primer: M13 Forward POLYA=No. Location/Qualif. 1. 588 /organism="Homo /mol_type="mRNA /db xref="taxon //clone="Iaxon	/lab_host="DH10] /clone=lib="NCI] /note="Vector: Inchests site NCI_CGAP_Sub4 11 the NCI_CGAP_Lost
n 5.1.6 Compugen Ltd. Search time 2523 Seconds	<pre>i909.804 Million cell updates/secgctagcgtcgacgcatgccg 458</pre>	700 residues parameters: 68479088			edicted by chance to have a ree of the result being printed, all score distribution.	AW207707 UI-H-BI2- BE218982 hv47a07.x AI912784 we13f07.x BE671554 we53h07.x BE669962 7e27908.x BE873976 601484045 BX111836 BX111836 CF341802 TGESTZYJ4 CF370966 TGESTZYJ5	CF370833 TGESTZYJS CD369973 UT-H-FTI- BUG34911 UT-H-FTI- BF938995 7r03f11.x CA307828 UT-H-FTI- CA307828 UT-H-FTI- CA307828 UT-H-FTI- AA995402 CF74f05.8 CF614774 (CES009198 CF614774 (CES009198 CF614774 (CES009198 CB430266 606148 MA CD367244 UT-H-FTI2- BM539160 hb05e10.9 AW951121 EST363191 AI677936 wc88f12.x AW784714 Zb77908.9
GenCore version Copyright (c) 1993 - 2005 OM nucleic - nucleic search, using sw model Run on: March 11, 2005, 15:19:06 ; Se	Title: VS-10-723-083-1 Perfect score: 458 Sequence: 1 cggcccgggatgcaccacca Scoring table: IDENTITY_NUC Gabon 10.0 . Gabext 1.0	.44 segs, 19032134700 satisfying chosen para	Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: gb_est1:* 2: gb_est2:* 3: gb_htc:* 4: gb_est3:* 5: gb_est3:* 6: gb_est5:* 7: gb_est6:* 9: gb_gss1:*	Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score d. SUMMARIES * Result Ouery No. Score Match Length DB ID	276.8 60.4 588 276.8 60.4 666 1 276.8 60.4 666 1 276.8 60.4 695 2 276.8 60.4 895 2 276.2 60.3 658 5 273.5 59.1 598 7	10 268.8 58.7 585 7 CF370833 11 264.8 57.8 718 6 CD369973 12 258.8 56.5 701 5 BU633411 13 256.4 56.0 565 2 BF938995 14 243.6 53.2 666 6 CA307828 15 230.8 50.4 651 6 CD368851 17 208.6 45.5 561 6 CB457551 18 207.2 44.2 511 6 CB45754 19 202.4 44.2 511 6 CB45754 20 200.2 43.7 608 6 CD367244 21 197.2 41.7 352 4 BM539160 22 191.2 41.7 336 2 AW951121 23 176.6 38.6 549 1 AL677936 24 175.2 38.3 423 2 AW784714

BG236310 naf26a07. AA361336 EST71529 BG236058 naf21h12. BB533718 BB533718 CB430980 606916 MA CP370895 TGESTZ955 BX521029 BX521029 A1180669 uc47d08.r BB664267 BB664267 A112.1878 ud43zd1.r CR052250 Forward 5 BE636680 rockefell AG112609 Pan troggl BQ620656 Talr1135H CF341980 TGESTZ955 AL053013 DC080phil CW010233 ZMMBLG01 CF341168 TGESTZ954 CG333578 CGMMB73TV CL959970 OSIFCC036	ALIGNMENTS MAZO7707 10.588 bp mRNA linear EST 02-DEC-1999 U1-H:DI2-agg-e-09-0-UI.s1 NCI_CGAP_SUD4 Homo sapiens CDNA clone INAGE:2724184 3', mRNA sequence. MAZO7707 MAZO7707 MAZO7707 MAZO7707 MAZO7707 G1:6507203 Homo sapiens (Numan) Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo. MAZO7707 MAZO7
BG236310 AA361936 BB533718 BB533718 CB430980 CF370885 A1121878 CR05250 BB664267 A121878 CR05250 BC63260 CC339578 CC339578 CC1959870	ALIGNMENTS 588 bp 1.6507203 (human) tazoa; Chordata; Crani heria; Primates; Catax 0.588) 1./www.ncbi.nlm.nih.go er Institute, Cancer of er and trauberg, Ph.D. rt Strausberg, Ph.D. rt Strausberg, Ph.D. rt Strausberg, Ph.D. remail.nih.gov in Gland, Not I sit ernal to the message. one distribution: Not I gov/bbrp/image/image.h 13 Forward tion/Qualifiers 5888 5888 5888 687 1997) rt Strausberg, Ph.D. rt Gond I sit gov/bbrp/image.h 13 Forward tion/Qualifiers 5888 5888 5888 5888 5888 5888 5888 58
531 623 623 623 623 623 704 704 705 705 705 705 705 705 705 705	AM207707 WITH-BIZ-age-e-09-0-UI.81 W IMAGE:2724184 3', mRNA seque AW207707.1 GI:6507203 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (buheria') Primates Eukaryota; Metazoa; Chordat. Mammalia; Butheria'; Primates I bases 1 to 588) NCI-CGAP http://www.ncbi.nl) NCI-CGAP http://www.ncbi.nl) NCI-CGAP http://www.ncbi.nl) NCI-CGAP http://www.ncbi.nl) NCI-CGAP http://www.ncbi.nl) Contact: Robert Strausberg, Email: Cgapbs-remail.nlh.go Oligo-dT track not found, Nis likely internal to the mage. Soares Lab Clone distributianformation can be found the www.bio.llnl.gov/bbrp/fmage. Soares Lab Clone distributianformation can be found the www.bio.llnl.gov/bbrp/fmage. POLYA=NO. Location/Qualifier. Josephylinker: Site 1 Not CGAP Colo. NCI NOT CGAP Sub libr. NCI NOT CGAP Sub Sub library mixture of 21 norm Ilbraries NCI CGAP NCI CGAP Lym2, NCI NCI CGAP Lym2, NCI NCI CGAP Libra, N
1166 1167 1179	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AW207707 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT COMMENT

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source
                 ORGANISM
                                                                                                            REFERENCE
AUTHORS
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NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI CGAP Kid3 pool 1: LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDS 132376-1323911, 1456008-1456775, 1500552-1502855) NCI CGAP Kid5 pool 1: LLAM 3338-3342, 372-3725, 3778-3778 (IMAGE CloneIDS 1323912-1325811, 1471368-1472993, 1492104-1493255) NCI CGAP Lu5 pool 1: LLAM 3318-3355, 3851-3854 (IMAGE CloneIDS 144920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1: LLAM 3164-1167, 3716-3720, 3733-3735 (IMAGE CloneIDS 1476743) NCI CGAP CONTROLS 125064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1: LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Col pool 1: LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 985608-986759, 1144584-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996); Normalization and control in the control in 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 400
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Discovery. Genome Research 6, 791-806.]
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Pred. No. 7e-50;
0; Mismatches 97; Indels 0
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Best Local Similarity 77.5%;
Matches 335; Conservative (
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BE218982 660 bp mRNA linear EST 03-JUL-2000 hv47a07.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3176532 3' similar to gb:MI1220 GRAUULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN); mRNA sequence.

DEFINITION

BE218982 BE218982.1 GI:8906300 EST.

ACCESSION VERSION KEYWORDS SOURCE

Homo sapiens (human)

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/d_one="twdgE:317632"
/tissue_type="carcinoid"
/tissue_type="carcinoid"
/lab_hofe="MIDE"
/clone lib="NCI CGAP Lu24"
/note="organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu2 seperaed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing Arrayed by: Greg Lennon, Ph.D. DNA Sequencing Center DNA Sequencing Content Clone distribution: NII-GAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 445.
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Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. L (bases 1 to 660)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
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Tumor Gene Index

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck; M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primar: -40UP from Gibco

High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE671554 1NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3286237 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                            369 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 428
                                                                                          308
                                                                                                                                  368 GCTTCAAGGAGAACCTCCAAGGACTTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
        189 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 248
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGCCCCGCTCACCATGATGGCGTCCCACTACA
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BE671554.1 GI:10032095
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BE671554
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 743 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 447.
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1 (bases 1 to 666)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                           FACTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

    .666
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:2340997"
                                                                                                                                                                                                                   AI912784
AI912784.1 GI:5632639
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429 TCCAGGAGTGAG 440
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Unpublished (1997)
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modified polylinker; Plasmid DNA from the normalized library NCI CGAP LuS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 114920-141791 and 1520904-1522439). Subtraction by Bento Soares and M. Patima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE873976 895 bp mRNA linear EST 20-OCT-2000 601484045F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886571 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTCAACCTCTCCCGCGACACCGCCGCGGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 895)
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencial by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM9663 row: j column: 12
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Homo sapiens
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Matches 335; Conservative
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Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
    Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.
    CDNA Library Preparation: M. Bento Soares, Ph.D.
    CDNA Library Arrayed by: Greg Lennon, Ph.D.
    DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: infoelunge: llni.gov
    Seq primer: -40UP from Gibco
    High quality sequence stop: 456.
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                                                                                                        68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 695)
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/lab_host="DH10B"
/clone lib="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with
        GGATGCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCCAGCGCGCA
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                          368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTGTGATCCCGTTCGACTGCTGGGAGCCGG
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/db_xref="taxon:9606"
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                                            /organism="Homo sapiens"
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/mol type="mRNA"
/db xref=taxon:9606"
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/note="Organ: lung, Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:1 kb. Library constructed by Life
Technologies."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Radelof, U., Schneider, D. and Korn, B.
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Unpublished (2003)
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Pred. No. 7.1e-50;
0; Mismatches 97; Indels 0
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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ity sequence stop: 711.
Location/Qualifiers
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Best Local Similarity 77.5%;
Matches 335; Conservative
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Homo sapiens
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High quality
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/issue_type="cortion;" invariants.
/lab host="DHIOB"
/lab host="DHIOB"
/lab host="DHIOB"
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/note="Corgan: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified cloned into the Not I and Soarse and M. Fatima Bonaldo. "
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RZPD; IMAGD998C104061.

RZPDLis I.M.A.G.B. CDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Rabbnerweg 6, D-14059 Berlin, Germany
Tel: 449 30 32639 101
Fax: 449 30 32639 101
Fax: 449 30 casiable royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq prin
increar RZPD (clone@rzpd.de) for further information. Seq prin
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.3%; Score 276:2; DB 5;
82.3%; Pred. No. 9.5e-50;
ive 0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .658
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998C104061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439
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Best Local Similarity 82.3
Matches 317; Conservative
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φ

307

427

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/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_txef="texaon:5811"
/clone="Toxoflasty;58612.y1"
/dev_stage="Tachyzoite"
/dev_stage="Tachyzoite"
/lab_host="ElectroTen Blue cells (Stratagene)"
/lab_host="ElectroTen Blue cells (Stratagene)"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/colne_lib="Tg CAST Tachyzoite cDNA Library"
/colne_lib="Tg CAST Tachyzoite cDNA Library was constructed by Reliang Tang, and Robert Cole at Washington University.
CDNA was synthesized from poly(A)+ mRNA using the template-switching PCR method (SWART CDNA Kit, BD Blossioness). First strand cDNA was reverse transcribed using the CDS III/3' primer and a 5' template switch primer (Smart IV primer). The product of the first strand synthesis was PCR amplified using the same primer set and the fragments were digested with Sfil. The fragments were size selected, ligated into a modified pBluescript vector (obtained from Michael Mhite, Montana State University)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF370966
592 bp mRNA linear EST 27-AUG-2003
TGEST2y158e12.y1 TG CAST TAChyzoite cDNA Library TOXOPLABAMA GONDLI
CDNA clone TGEST2y158e12.y1 S' similar to SW:CSF2 HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ; MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq primer: -40UP from Gibco.
Location/Qualifiers
     217 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 276
                                                                                                                                                                                                              308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCCACCTAGATCATCACCTTCGAGA 367
                                                                                                                                                                                                                                                                                                                                                                                                             337 AGCAGCACTGCCATCCAAACCCCGGAAACTTCCTGTGCAACCCCAGACTATCACCTTGAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sarcocystidae; Toxoplasma.

1 (bases 1 to 592)

Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hallar, L., Kucaba, T., Theising, B. Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tasgareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.

Copiasma EST Project
Unpublished (2001)
                                                                                                                                                           248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGCCCGCTCACCATGATGGCGTCCCACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
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CF370966
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//do_zref="taxon:5811"
//do_zref="taxon:5811"
//doze="Toxoplasma gondii"
//doze="Toxon:5811"
//doze="Toxon:5811"
//doze="Toxon:5811"
//doze="Toxoplasma gondii"
//dov stage="Tachyzoite"
//dov stage="Tachyzoite"
//dov stage="Tachyzoite"
//dox old ib="Toxoplasma"
//doze="Toxoplasma"
//doze="Toxopla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seg primer: -40UP from Gibco.
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GGCCGCCTCGGCCACCGACCGT, where n=3-4 G nucleotides.
WARNING: the library contains a small percentage of CDNAs
derived from the human host cells. Library materials
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                                                                                                                                                                                                                                                                                                                                           Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Golffton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvill, R., Ronko, I., Kannedy, S., Maguire, L., Waterston, R. and Wilson, R. Toxoplasma EST Project Unpublished (2001)
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Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1810
Fax: 314 286 1810
Email: toxo@watgon.wustl.edu
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Sarcocystidae, Toxoplasma.

    (bases 1 to 584)

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          GI:33831915
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Matches 334; Conservative
                                                                                                                                                      Toxoplasma gondii
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          CF341802.1
                                                                                                         Toxoplasma
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JOURNAL
COMMENT
VERSION
KEYWORDS
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containing directional Sfil sites, and electroporated into ElectroTen Blue cells. Vector: Sfil sites were added to the multiple cloning region of pBluescript SK+ between the BamHI/RcoRI sites. The modified polylinker has the following sequence: 5'GAATTCGGCCATTACGGCC (G)n-- insert--GOCCGCTCGGCCCACGGATCC3' where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."
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585 bp mRNA linear EST 27-AUG-2003
GEST27/55612.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
cDNA clone TgEST27/55612.y1 5' similar to SW:CSF2 HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
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1 (bases 1 to 585)
Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Matin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Kniter, E., Bennett, J., Franklin, C., Tasgareishvili, R., Ronko, I., Konpdjasma BST Project
Toxoplasma BST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                           CGCCCAGCCCAGCAGGCAGGCATGTGAATGCCATCCAGGAGGCCCGGCGTC
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Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
                                                                                                                                                                                                                      Query Match 59.7%; Score 273.6; DB 7; Length 592; Best Local Similarity 77.1%; Pred. No. 3.5e-49; Matches 333; Conservative 0; Mismatches 99; Indels 0
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CF370833.1 GI:34318079
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/dev stage="ITachyzotte"
//dev stage="ITachyzotte"
//dev stage="ITachyzotte"
//deb_host="ElectroTen Blue cells (Stratagene)"
//clone lib="Tg CAST Tachyzotte cDNA Library
//note="Vector: Modified pBluescript (pBS Sk+); Site 1:
//note="Vector: Modified pBluescript was constructed by
//note="Vector: Modified pBluescript"
//note="Vector: Modified by Modified pBluescript was constructed by
//note="Vector: Trand cDNA was reverse transcribed
//note="Vector: Transcribed bBluescript"
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//note="Vector: Transcribed bBluescript"
//note="Vector: Transcript"
//note="Vector:
                                    Tel: 314 286 1800

Fax: 314 286 1810

Email: toxo@watson.wustl.edu

Contact David Sibley (toxoest@borcim.wustl.edu) for further

information relating to organism, libraries, or clone availability.

Seg primer: -40UP from Gibco.
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Parkway, Box 8501, St. Louis, MO 63108,
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Best Local Similarity 76.4%; Pred. No. 3.8e-48;
Matches 330; Conservative 0; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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/clone="TgESTzyj55e12.y1"
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/downer="Ut-H-F71-Nebc" / devenor-Out" / devenor-William / devenor-William / devenor-William / devenor-William / devenor-William / devenor-Outen / devenor-William / denovirus / denovirus / denovirus / defenor-William / denovirus / denovirus / denovirus / defenor-William / denovirus / denovirus
                                                                           CD369973 718 bp mRNA linear EST 05-AUG-2004 UI-H-FTI-bke-o-08-0-UI.81 NCI CGAP_FTI Homo sapiens CDNA clone MIH-FTI-bke-o-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thtp://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this CDNA
Seq primer: M13 FORWARD
PODYA=YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cançer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (1997)
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CD369973/c
                                                                                                                                   DEFINITION
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@wiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-46, >AT_rich#Low_complexity 60-129,
> (TAAA) n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 TGTACAAGCAGGCCTCCGCGCGCCTCACCAAGCTCAAGGCCCCGCTCACCATGATGG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 CGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGGCCACCCAGATCA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 TCACCTTCGAGAGAGCTTCAAGGAGAACCTCCAAGGACTTCCTCCTCGTGATCCCGTTCGACT 415
                                                                                                                                                                                                                                                            718 caccedecedercececeáceceacacacadedecericadadearardadarecericade 659
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                                                                                                                                                                                                                                                                                                            116 AGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 AAGTCATCTCAGAAATGTT-GACCTCCCAGAAGCCGACCTGCCTACAGACCCGCCTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 CCAGCCACTACAAGCAGCACTGCCTCCAACCCGGAAACTTCCTGTGCAACCCAGATTA
                                                                                                                                                                                                                    56 CGCCAGCGCGCAGCCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGG
                                                                                                                                                                 1; Gaps
                                                                                                                    Length 718;
TAG_TISSUE=Human Lung Alveolar Macrophage
                                                                                                                 Query Match 57.8%; Score 264.8; DB 6; Length Best Local Similarity 82.3%; Pred. No. 2.8e-47; Matches 316; Conservative 0; Mismatches 67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                      TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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BU633411.1 GI:23300666
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Best Local Similarity
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465 AGTCCAGGAGTGAG 478
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                                                                                             /doceant bear interested by the state of the
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 565)
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                                                         /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone="UI-H-FL1-bgu-l-15-0-UI"
/tissue_type="Cell lines"
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Matches 307; Conservative
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REFERENCE

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/ tlssue type="carcinoid"
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                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Esmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 CAAGCAGCACTGCCCACCGACCCCGGAGACTCCTGCGCCACCAGATCATCACCTTCGA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 CGCCCAGCCCCAGCAGCCCGTGGGAGCATGTGAATGCCATCACAGGAGGCCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GGATGCACCACCACCACCACCACTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 GCCCGAGCCCGTCCACCCAG-CCGTGGAGCACGTGAACGCGATC-CAGGAGGCCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 GCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 CGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 GAGCTTCAAGGAGAACCTCCAAGGACTTCCTCGTGATCCCGTTCGACTGGGAGCC
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Pred. No. 1.9e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                           infooimage llnl.gov
Seg primer: -400P from Gibco
High quality sequence stop: 497.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGCAGGAGTGAG 439
                                                                                 Unpublished (1997)
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Best Local Similarity 77.43
Matches 336; Conservative
                                                          Tumor Gene Index
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228

288 486 426

ACCESSION

VERSION

JOURNAL

FEATURES

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CD368851 661 bp mRNA linear EST 05-AUG-2004 UI-H-FT1-bjx-m-02-0-UI.sl NCI CGAP_FT1 Homo sapiens CDNA clone NL-FT1-bjx-m-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 CAGAICATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCG 408
                                                                                                                                                       289 ATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGAACCCCGGAGACCTCCTGCGCCACC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 CAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 661)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                 169 ACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGC
                                                                                                                                                                                                                                                                       229 CTCGAGCTGTACAAGCAGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGCCCGCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 ATGATGGCCAGCCANTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACC
                                                                                                              0; Gaps
                                                                Query Match 53.2%; Score 243.6; DB 6; Length 666; Best Local Similarity 83.4%; Pred. No. 1.1e-42; Matches 276; Conservative 0; Mismatches 55; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            > (TAAA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 TTCGACTGCTGGGAGCCGGTGCAGGAGTGAG 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
TAG_SEQ=GCCCATGCCG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD368851
CD368851.1 GI:31152941
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Seq primer: M13 FORWARD
POLYA=Yes.
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Best Local Similarity
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                               Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

Email: charary preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this cDNA

sequence: 1-50, >AT_rich#Low_complexity 64-133,

> (TAAA) Misimple_repeat

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA307828 666 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bhx-f-10-0-UI.sl NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bhx-f-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .66
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/clone="UI-H-FT1-bhx-f-10-0-UI"
/rissue_type="Alveolar Macrophage"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                  CA307828.1 GI:24470882
                                                                                                                                                                              Homo sapiens (human)
                                                                                                                CA307828
                                                                                                                                                     KEYWORDS
SOURCE
ORGANISM
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  RESULT 14
CA307828/c
                                                                DEFINITION
                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
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NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, others pamples were pooled for library construction. Control 0 hours; control 3 hours; Klebsiella moi 10, 24 hours; Rtabsiella moi 10, 24 hours; Rtabsiella moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Ad vector + LPS 3 hours; wt adenovirus moi 500, 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hou
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TAG LIB=UI-H-FT1
TAG SEQ-GGCCATGCCG"
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Query Match 50.4%; Score 230.8; DB 6; Length 661; Best Local Similarity 83.5%; Pred. No. 6.7e-40; Matches 273; Conservative 0; Mismatches 53; Indels 1.

ORIGIN

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Search completed: March 11, 2005, 17:24:17 Job time : 2532 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                              - nucleic search, using sw model
                                                                              OM nucleic
                                                                                                                      Run
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March 11, 2005, 09:51:36; Search time 420 Seconds (without alignments) 6455.337 Million cell updates/sec ë

US-10-723-083-1 Perfect score:

1 cggcccgggatgcaccacca......gctagcgtcgacgcatgccg 458 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

genesegn2003cs:* genesegn2003ds:* geneseqn2002bs:*geneseqn2003as:*geneseqn2003bs:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:*geneseqn2002as:* N_Geneseq_16Dec04:* 1: qeneseqn1980s:* geneseqn1980s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004as:* genesegn2004bs:*

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	90	7	7	~	12	12	12	~	٣	9	12	~	٣	9	12	~	m	9	12	~	٣
	* Query Match Length DB	905	896	386	435	435	435	777	777	777	777	402	402	402	402	822	822	822	822	903	903
	% Query Match	69.7	69.5	68.8	68.3	67.9	62.1	61.9	61.9	61.9	61.9	61.8	61.8	61.8	61.8	61.4	61.4	61.4	61.4	61.4	61.4
	Score	319.2	318.4	315	312.6	311	284.4	283.6	283.6	283.6	283.6	283	283	283	283	281	281	281	281	281	281
	Result No.		~	m	4	s	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20

Abx00023 Human int Adj14278 DNA relat Adf31962 Human GM- Adf31969 Human GM- Aan90383 Synthetic Aan90274 Synthetic Adj16719 Human gra Adj4018 Granulocy Adj10714 Human Gra Adg4018 Granulocy Adj10387 Reference Aan60364 Human Gra Adg4865 Clone pcD Aaa35017 Human ara	A4721139 Human low A472817 Nucleotid A529683 Human nuc Ab420682 Human pul A47725 H672-GM-C A435020 Human ade A4721142 Human ade A52142 Human low A5296836 Human nuc Ab420685 Human nuc Ab420685 Human nuc Abx63509 Human cDN
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3275275	8 2 11 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
903 903 1538 1538 415 415 2211 763 763 787 787	789 789 789 789 2385 5115 5115 5115 5115
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281 281 281 281 281 281 281 281 281 281	276.8 276.8 276.8 276.8 276.8 276.8 276.8 276.8
	33 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer; ds. DNA fragment of pAEO-GMCSF encodes granulocyte macrophage colony stimulating factor (GM-CSF) H. 89EP-00113607. 88CA-00572956. AAQ03221 standard; DNA; 905 (first entry) (CANG-) CANGENE CORP. gb. Streptomyces 24-JUL-1989; 25-JUL-1988; 12-JUL-1990 31-JAN-1990 EP352707-A. AAQ03221; RESULT 1 AAQ03221

Garvin RT, Malek LT;

WPI; 1990-031296/05.

gene expression system directing secretion of protein in Streptomyces contg. structural gene, esp. for granulocyte macrophage colony stimulating factor, and regulatory sequence.

Disclosure; Fig 4; 39pp; English.

GM-CSP, or a wide range of other proteins, is secreted in unglycosylated form, with correctly positioned intramolecular disulphide bonds and full biological activity. pABC.GMCSF contains the BamHI HindIII fragment with an aminoglycoside phosphorransferase promotor and the protease B-endo H hybrid signal peptide. GM-CSF is potentially useful in cancer treatment

Sequence 905 BP; 131 A; 367 C; 298 G; 109 T; 0 U; 0 Other;

Gaps

; 0

Indels

Length 896; 0 Other;

DB 2;

Score 318.4; DB 2 Pred. No. 8.1e-49; 0; Mismatches 41

69.5%; 89.3%;

G; 106 T; 0 U;

C; 291

114 572 174 632

234

294

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633 gaddicarcrogadardricdacrrocaddadcocacgrocordcocadaccocacago 692
                                                                                                                                                                                                                                                                                  GCGCCAGCGCGCAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG
                                                                                                                GCCCCCGCCCGGTCGCCTCGCCGTCGACCCTGGGAGCACGTCAACGCGATCCAG
                                                                                                                                                                          CTGTACAAGCAGGCCTCCGCGCGCAGCCTCACCAAGCTCAAGGGCCCCGCTCACCATGATG
                                                                                                                                               GAGGCCCGCAGGCTCCTCTCCCCGCGACACCGCCGAGATGAACGAGACCGTG
                                                                                                                                                                                                    GAGGIGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG
            Sequence 896 BP; 135 A; 364
                                                                 Matches 343; Conservative
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                                                      Similarity
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                                       Query Match
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                                                                                                                                                                                                                                                                                                   742 Aggegecegergaccargargecerceaeracaaacageaergeceeeeeeeeegaaga 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GM-CSF, or a wide range of other proteins, is secreted in unglycosylated form, with correctly positioned intramolecular disulphide bonds and full biological activity. DAPO.GMCSF contains the BamHI HindIII fragment with an animoglycoside phosphotransferase promotor and the protease B signal peptide. GM-CSF is potentially useful in cancer treatment
                                                      94
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                                                                                                                               562 AGCACGTCAACGCGATCCAGGAGGCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG
                                                                                                                                                                                                                                              682 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA
                                                                       95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCCGCCG
                                                                                                                                                               CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT
                                                                                                                                                                                        622 ccaadardaacdadaccardaaccraarcrccaacargrrccacrrccacacacaccaccr
                                                                                                                                                                                                                     GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA
                                                                                                                                                                                                                                                                           AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCGGAGA
                                                      CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCAGCCGTGGG
                            Gaps
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0
 Score 319.2; DB 2; Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                  862 TCCTCGTGATCCCCTTCGACTGCGGAGCCGGTGCAGGAGTGA 905
                                                                                                                                                                                                                                                                                                                                                                                    TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
                           Indels
                            53;
              5.8e-49;
                         0; Mismatches
              Pred. No.
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69.7%;
86.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ03220 standard; DNA; 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragment of pAPO-GMCSF stimulating factor (GM-CSF)
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            Best Local Similarity 86.9 Matches 351; Conservative
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GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCCAGATC 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression system directing secretion of protein in Streptomyces contg. structural gene, esp. for granulocyte macrophage colony stimulating factor, and regulatory sequence.
              granulocyte macrophage colony stimulating factor
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                                                                                                                                                                                                                                                                                                      Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer;
                                                                                                    TGCTGGGAGCCGGTGCAGGAGTGA 438
                                                                                                                 TGCTGGGAGCCGGTGCAGGAGTGA 896
                                                                                                                                                                                          BP.
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                                                                                                                                                                                        AAQ03219 standard; DNA; 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA sequence comprising a codon optimized sequence encoding a mammalian granulocyte macrophage-colony stimulating factor, useful as an adjuvant for enhancing an immune response of a mammal to preventive or
                                                                                   83
                                                                                                                                             264 TGCCCCCCCACGCCGGAGACGTCGTGCCCCACCCAGATCATCACGTTCGAGTCGTTCAAG
                                                                                                             GATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGC
                                                                                                                                                                     GGCAGCCTCACCAAGCTCAAGGCCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCAC
                                                                                                                                                                                GGCAGCCTCACCAAGCTCAAGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCAC
                                                                                  CCGTCCACCCACCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAAC
is potentially useful in cancer treatment
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       stimulating factor; GM-CSF;
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                                 Length 386
                                                 30; Indels
               Seguence 386 BP; 73 A; 141 C; 116 G; 56 T; 0 U; 0 Other;
                                Score 315; DB 2;
Pred. No. 3.4e-48;
0; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                      mammalian granulocyte macrophage-colony
Immunostimulant; Cytostatic; vaccine; ds
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                                                                                                                                                                                                                                                                                                                                    BP.
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                               Query Match
Best Local Similarity 91.7%;
Matches 333; Conservative
activity, GM-CSF
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                                                                                                                                                                                                                                                                                                                                                                                      Human GM-CSF
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biological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a DNA sequence comprising a codonoptimized sequence encoding a mammalian granulocyte macrophage-colony stimulating factor (GM-CSF), is new, where the codon optimized sequence is different from the corresponding wild type GM-CSF encoding DNA, where expression of the mammalian GM-CSF. The method is useful as an adjuvant in gene therapy or in vaccination for enhancing an immune response of a mammal to a preventive or therapeutic vaccine, is also useful for treating cancer or for effecting gene therapy. Use of the DNA sequence comprising a codon optimized sequence encoding a mammalian granulocyte macrophage-colony stimulating factor as an adjuvant results in improved gene sequence. The present sequence represents human GM-CSF associated encoding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAGCTGTACAAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGCCCGCTCACCATGATGGCGTCCCACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCCACACATCATCATCATCTTCGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 435 BP; 94 A; 151 C; 128 G; 62 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 312.6; DB 12;
Pred. No. 9.3e-48;
0; Mismatches 74;
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Immunostimulant; Cytostatic; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.8%;
Matches 357; Conservative
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ADQ76023 standard; DNA; 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a DNA sequence comprising a codonoptimized sequence encoding a mammalian granulocyte macrophage-colony stimulating factor (GM-CSF), is new, where the codon optimized sequence is different from the corresponding wild type GM-CSF encoding DNA, where a codon in the codon optimized sequence has been altered to enhance the expression of the mammalian GM-CSF. The method is useful as an adjuvant in gene therapy or in vaccination for enhancing an immune response of a mammal to a preventive or therapeutic vaccine, is also useful for treating cancer or for effecting gene therapy. Use of the DNA sequence comprising a codon optimized sequence encoding a mammalian granulocyte macrophage-colony stimulating factor as an adjuvant results in improved adjuvant activity when expressed in vivo compared with the native GM-CSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCCGCCTCGAGCTGTACAAGCAGG
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Pred. No. 1.8e-47;
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82.6%;
03-JUL-2003; 2003WO-US020908
                                                03-JUL-2002; 2002US-00188056
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Matches 356; Conservative
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                                                                                               (VAXI-) VAXIM INC
                                                                                                                                          Lai W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method of optimising a coding sequence for expression of a protein, based on the amino acid sequence of the protein. This involves the use of a computer to generate a test sequence with m optimisation positions determined for a defined region, in which positions the codon usage is varied. The optimum codon usage at such positions is determined by means of a power function. The steps are relierated with different regions of the sequence, with the optimised codons previously identified being left unchanged during subsequent steps. The method can be used for expression of proteins. The present sequence is a codon optimised version of the human GM-CSF coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer optimization of a nucleotide sequence for a protein comprises evaluating test sequences with a quality function to determine the
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                                                                                                                                   ds; gene; human; GM-CSF; codon optimisation; protein production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 284.4; DB 12; Length 435; 
Pred. No. 1.2e-42; 
0; Mismatches 61; Indels 0;
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                                                                     Human GM-CSF codon optimised coding sequence
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Best Local Similarity 84.0%;
Matches 321; Conservative (
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352 ATCACCTTCGAGAGCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGAT 411
                                                                                                                                                                                                                                                                                                                                                                                       Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine; mutant; mutein; fusion protein; linker; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein has the usual activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Easton AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion proteins comprising a human interleukin-3 variant, a linker sinterleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caparon MH,
Thomas JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0.U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Braford-Goldberg SR,
Olins PO, Paik K,
                                                                                                                                                                                                                                                                                                                                          pMON13022 DNA encoding IL-3 fusion protein.
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                                                                                         433
                                            TGCTGGGAGCCGGTGCAGGAGT
                                                                                       412 recredeacccerecadar
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                                                                                                                                                                                                                                                                                                (first entry)
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Mckearn JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-283774/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bauer CS,
Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                            415
                                                                                                                                                                                                                                                     AAQ97169;
                                                                                                                                                         RESULT 7
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153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methods have been developed for treating haematopoietic disorders with fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-3) variants or mutant proteins (muteins) fused with secondary colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating hematopoietic disorders with fusion proteins comprising mutated interleukin-3 fused with secondary colony stimulating factors or other interleukin-3 variants.
                                                                                                                                                                                                                                                                                                                                                                676 ACTICCTGIGCAACCCGGATTATCACCTTTGAAGTTTCAAAGAGAACCTGAAGGACTTC
376 TCTGGCGGCGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG
                                                                                                                         154 GCCGAGATGAACGAGCGTGGAGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC
                                                                                                                                                                                                                    556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC
                                                                                                                                                                                                                                                                                          616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAAACCCGGAA
                                                       GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC
                                                                                        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT
                                                                                                                                                            496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT
                                                                                                                                                                                                                                                                     274 AAGGGCCCGCTCACCATGATGCCGTCCCACTACAAGCAGCACCTGCCCACCGACCCCGGAG
                                                                                                                                                                                                                                                                                                                                          334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:55.
                                                                                                                                                                                               214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGGAGCCTCACCAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine; colony stimulating factor; haematopoietic growth factor; lymphokine; fusion protein; haematopoietic disorder; infection; cancer; radiation therapy; chemotherapy; bone marrow suppressive drug; bone marrow activation; blood cell activation; blood transplant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin-3 mutant containing fusion protein DNA
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Caparon MH,
                                                                                                                                                                                                                                                                                                                                                                                                                394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bb
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95WO-US001185.
95US-00411795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-160368/14.
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06-APR-1995;
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Gaps

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Score 283.6; DB 2; Length 777; Pred. No. 1.6e-42; 0; Mismatches 74; Indels 0

Query Match
Best Local Similarity 81.6%;
Matches 328; Conservative

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and/or haematopoietic colony stimulating factors) or other interleukin-3

c variants with or without a linker. The methods may be used in vivo to

treat haematopoietic disorders resulting from bacterial, viral and fungal

infections, cancer radiation therapy, chemotherapy or bone marrow

c suppressive drugs. They may also be used in vitro to stimulate bone

marrow and blood cell activation and growth prior to infusion of the bone

c marrow and blood transplants into patients. IL-3 is a haematopoietic

c growth factor which has the property of being able to promote the

survival, growth and differentiation of haematopoietic cells. The fusion

c molecules are characterised by possessing the usual activity of both of

their constituent peptides and further by having a biological or

c physiological activity greater than the additive function of the IL-3 or

second CSF alone (i.e. the peptides act synergistically). Their activity

c may also be further enhanced by the mutations they comprise. The

c variations may further reduce undesirable side effects associated with IL

c used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTICCIGIGGAACCCAGAITAICACCIITIGAAGIITICAAAGAGAACCIGAAGGACIIC 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCGGGGACACCGCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCGGAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 TCTGGCGGCGCCTCCAACATGGCACCGGCTCCTTCCCCCGTCCCCGTCTACCCAGCCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 GAACACGIGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 61.9%; Score 283.6; DB 3; Length 777; Best Local Similarity 81.6%; Pred. No. 1.6e-42; Matches 328; Conservative 0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919
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of

Easton AM;

Caparon MH, Thomas JW;

Braford-Goldberg SR, Olins PO, Paik K,

Abrams MA, Mckearn JP,

SC, BK,

Bauer Klein WPI; 2002-749206/81

cultured cells.

92US-00981044. 93WO-US011197. 94US-00192325. 95WO-US001185. 95US-00411795.

95US-00446872

06-JUN-1995;

(SEAR) SEARLE & CO G D.

96US-00762227

09-DEC-1996;

24-NOV-1992 04-FEB-1994 04-FEB-1995 06-APR-1995

20-AUG-2002

Unidentified. US6436387-B1. Ex vivo expansion of stem cells, for enhancing transduction efficiency cultured stem cells, comprises culturing stem cells in growth medium having mutant interleukin-3, and hematopoietic factor, and harvesting

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Haematopoietic factor; GM-CSF, colony stimulating factor; CSF-1; ds, G-CSF, G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand; human growth hormone; B-cell growth factor; leukaemia, b-cell differentiation factor; eosinophil differentiation factor; stem cell factor; SCF; cyclic neutropenia, aplastic anaemia; thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome; systemic lupus erythematosus; SLE; myelodysplastic syndrome; myelofibrosis; Interleukin-3; IL-3; stem cell.
394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
                                     736 crecrrercárcecerrreacrecreseaseceasiceasidas 777
                                                                                                                                                                                                                                                            Human interleukin-3 associated DNA sequence #3.
                                                                                                                                     ABX00012 standard; DNA; 777 BP
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                               ABX00012;
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The invention relates to ex vivo expansion of stem cells, comprises culturing stem cells with a growth medium comprising a chimaera protein, and harvesting the cultured stem cells. The chimaera is based on a mutated human interleukin-3 (IL 3) sequence coupled to a haematopoietic factor (e.g. GM-GSF (colony stimulating factor), CSF-1, G-CSF, G-CSFS-17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16, filt3 ligand, human growth hormone, B-cell growth factor, B-cell differentiation factor, eosinophil differentiation factor and stem cell factor (SCF) via a peptide linker. The formula for the chimaera is given in the specification. Also included is a method for enhancing the efficiency of the transduction of cultured stem cells by a heterologous culturing the stem cells with a growth medium comprising the chimaera (c) culturing the stem cells with a growth medium comprising the chimaera (c) transducing DNA into cultured cells; and (d) harvesting the transduced cells; and enhancing the efficiency of the transduction of cultured stem cells by a heterologous gene. The method is also useful for treating a patient containing a haematopoietic disorder. The expanded haematopoietic cells are also useful in the treatment of cyclic neutropenia, aplastic anaemia, thrombocytopenia, idiopathic neutropenia, melodysplastic syndrome and myelofibrosis. The present sequence is an IL-3 mutant associated DNA sequence is an IL-3 mutant associated DNA sequence is an IL-3 mutant associated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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81.6%; Pred. No. 1.6e-42;
ive 0; Mismatches 74;
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nes 328; Conservative
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chimera protein, followed by harvesting of the cultured stem cells. The method of the invention has antianaemic, immunostimulant, immunosuppressive, immunomodulator, antiinflammatory, dermatological, immunosuppressive, cytostatic and neuroprotective applications and may be useful to target haemopoietic calls for gene therapy, preferably for treating patients, having a haemopoietic disorder characterised by decreased levels of system. The expanded ex vivo cells may be used to treat neutropenia, aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome, system: priodic neutropenia, Chediak-Higashi syndrome or myelofibrosis. The current sequence is that of a DNA related to the human interleukin-3 (IL-3) mutant protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin, hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
mutant; mutein; fusion protein; linker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGCACCCGGAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 TCCGGCATCGAGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCGTCCACCCAGCCGTGG
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                                                                                                                                                                                                                                                                                                Score 283.6; DB 12; Length 777;
Pred. No. 1.6e-42;
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81.6%;
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                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; dermatological; immunosuppressive; cytostatic; neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid; lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia; Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia; myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.
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                                                                                                                                                               ACTICCIGIGEAACCCAGAITATCACCTITGAAAGITICAAAGAGAACCIGAAGGACTIC 735
                                                                333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method whereby stem cells are ex vivo expanded via culturing the stem cells with a growth medium comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating aplastic anemia, involves culturing the stem cells with growth medium comprising chimera protein, and harvesting the cultured stem cells.
AAGGGCCCCCTCACCATGATGCCGTCCCACTACAAGCAGCACTGCCCACCGACCCGGAG
                                                                                              AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA
                                                                                                                                       ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell; antianaemic; immunostimulant; immunomodulator;
                                                                                                                                                                                                                   CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
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Olins PO, Paik K,
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95US-00411795.
95US-00446872.
96US-00762227.
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BRAFORD-GOLDBERG S
CAPARON M H.
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Mckearn JP,
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KLEIN B K.
MCKEARN J P.
OLINS P O.
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06-JUN-1995;
09-DEC-1996;
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A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human interleukin: 3 (hIL-3), R2 is a second colony stimulating factor (GSF) interleukin: 3 (hIL-3), R2 is a second colony stimulating factor (GSF) and specifically claimed examples are shown in AAM792358-R79335 and AAM79242-R79345. The fusion protein is made by recombinant DNA techniques. Specifically claimed examples of DNA recombinant DNA techniques. Specifically claimed examples of DNA recombinant DNA techniques of protein are shown in AAM7916-C97204 and AAM79222-097227. The fusion protein is used to increase haematopoietic sequences which encode these proteins are shown in AAM7916-C97204 and AAM79222-097227. The fusion protein is used to increase haematopoietic cell production. It is also useful as an IL-3 antagonist or as a discrete antigment fragment for production of antibodies useful in immunosassays and immunotherapy. Antagonists are used to block the growth of cartain cancer cells and in treatment of asthma. The fusion protein can also be used to stimulate bone marrow and blood cell activation and growth in vitro before infusion; and to treat diseases characterised by decreased levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic system. The protein has the usual activity of both its reduced undesired side effects
                                                                                                                                                                             Fusion proteins comprising a human interleukin-3 variant, a linker and interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
                           MH, Easton AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;
                        Caparon Mi
Thomas JW;
                        Braford-Goldberg SR,
Olins PO, Paik K,
                                                                                                                                                                                                                                                                                           Example 19; Page 183; 447pp; English.
                                                 Olins PO,
                                                                                                     WPI; 1995-283774/37.
                                                                                                                              P-PSDB; AAR79338
                        Bauer CS,
Klein BK,
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CAGGAGGCCCGCAGGCTCCTCTCTCCCGCGACACCCGCCGAGATGAACGAGACC 171 caddadeccedecercretaaaccreaeradadacacrecretadardardaaaca 120 231 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180 GAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGCCCCGCTCACCATG 291 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGCCCCCTTGACCATG 240 ATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAG 351 Arigiocagicactricaaggaggacricicactricaagggaaagtricitergaaggaaggaag ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCTTT 360 9 GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC 52 ATGGGGGCGAGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATC 1 Aridecaccedercerrececerecererraceasecereseaacacereaareceare ö Match 61.8%; Score 283; DB 2; Length 402; Local Similarity 83.2%; Pred. No. 2.1e-42; les 322; Conservative 0; Mismatches 65; Indels GACTGCTGGGAGCCGGTGCAGGAGTGA 438 241 352 412 361 61 121 181 292 Query Match 112 172 232 301 g 셤 임 ò 유 ò 8 ò

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AAA03771 standard; DNA; 402

RESULT 12 AAA03771 ID AAA0 XX

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Methods have been developed for treating haematopoietic disorders with fusion proteins comprising recombinant, mutated human interleukin-3 (hlu-5) variants or mutant proteins (muteins) fused with secondary colony stimulating fused with secondary colony stimulating factors) interleukin and/or haematopoietic colony stimulating factors) or other interleukin-3 cand/or haematopoietic colony stimulating from bacterial, viral and fungal infections, cancer radiation therapy, chemotherapy or bone marrow and blood cell activation and growth prior to influsion of the bone marrow and blood cell activation and growth prior to influsion of the bone marrow and blood cell activation and growth prior to influsion of the bone compressive drugs. They may also be used in vitro to stimulate bone marrow and blood cell activation and growth prior to influsion of the bone convert factor which has the property of being able to promote the convertium and differentiation of haematopoietic cells. The fusion molecules are characterised by possessing the usual activity of both of their constituent peptides and further by having a biological or physiological activity greater than the additive function of the IL-3 or second CSF alone (i.e. the peptides act synergistically). Their activity may also be further reduce undesirable side effects associated with IL and ANSASI30 to ANSASI30 to ANSASISO and ANSASISO to ANSASISO ANSASISO TO ANSASISO TO ANSASISO ANSASISO ANSASISO TO ANSASISO ANSASISO TO ANSASISO TO ANSASISO ANSASISO ANSASISO TO ANSASISO ANSASISO TO ANSASISO TO ANSASISO TO ANSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating hematopoietic disorders with fusion proteins comprising mutate interleukin-3 fused with secondary colony stimulating factors or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 ATGGCGCCAGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATC
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                                                                                                                                                  Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine; colony stimulating factor; haematopoietic growth factor; lymphokine; fusion protein; haematopoietic disorder; infection; cancer; radiation therapy; chemcherapy; bone marrow suppressive drug; bone marrow activation; blood cell activation; blood transplant; ds.
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83.2%; Pred. No. 2.1e-42;
ive 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Easton AM,
Caparon MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;
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                                                                                                      Human G-CSF mutant DNA sequence SEQ ID NO:176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Braford-Goldberg SR, Mckearn JP, Olins PO,
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95US-00411795.
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Best Local Similarity 83.29
Matches 322; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bauer SC, Abrams MA
Paik K, Thomas JW,
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                                                                                                                                                                                                                                                                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                 Synthetic.
AAA03771;
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Gracaacticararcacaaarcrirgaccricaggagccgacrigccracagacccgccric 180
                                                                                                                                                                     GAGCTGTACAAGCAGGCCTGCGGGCCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240
                                                                                                                                                                                                                                                               expansion of stem cells, for enhancing transduction efficiency of
                                                                                                               GAGCTGTACAAGCAGGCCTCCGCGCCAGCCTCACCAAGCTCAAGGCCCGCTCACCATG 291
                                                                                                                                                                                                                              ATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAG 351
                                                                                                                                                                                                                                                                                                                                                 ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; ds; G-CSF: G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand; human growth hormone; B-cell growth factor; leukaemia; B-cell differentiation factor; eosinophil differentiation factor; stem cell factor; SCF; cyclic neutropenia; aplastic anaemia; thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome; systemic lupus erythematosus; SLE; myelodysplastic syndrome; myelofibrosis; Interleukin-3; geem cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cultured stem cells, comprises culturing stem cells in growth medium
having mutant interleukin-3, and hematopoietic factor, and harvesting
GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC
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Thomas JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human interleukin-3 associated DNA sequence #77.
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Olins PO, Paik K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTGCTGGGAGCCAGTCCAGGAGTGA 387
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94US-00192325
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95US-00411795
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Mckearn JP,
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04-FEB-1994;
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06-APR-1995;
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BK,
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Klein )
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mutated human interleukin-3 (IL 3) sequence coupled to a haematopoietic cases. GM-CSF (colony stimulating factor), CSP-1, G-CSF, G-CSFS-1, C-CSF, G-CSFS-1, C-CSF, G-CSFS-1, C-CSF, G-CSFS-1, C-CSF, G-CSF, G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Match 61.8%; Score 283; DB 6; Length 40 Local Similarity 83.2%; Pred. No. 2.1e-42; nes 322; Conservative 0; Mismatches 65; Indels
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ADJ14388
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pMON13035 DNA encoding IL-3 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bauer CS, Abrams MA,
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                                                                                                                                                                                                                                                                               The invention relates to a novel method whereby stem cells are ex vivo expanded via culturing the stem cells with a growth medium comprising a chimera protein, followed by harvesting of the cultured stem cells. The method of the invention has antianaemic, immunostimular, immunosuppressive, cytostatic and neuroprotective applications and may be useful to target haemopoietic cells for gene therapy, preferably for treating patients chaemopoietic disorder characterised by decreased levels of mayoloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic system. The expanded ex vivo cells may be used to treat neutropenia, system. The expanded ex vivo cells may be used to treat neutropenia, system; clupus erythematosus, leukaemia, mediak-Higashi syndrome, systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or myelofibrosis. The current sequence is that of a DNA related to the human interleukin-3 (IL-3) mutant protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ATGGCGCCAGCGCAGCCCCAGCCCGTCCACCCAGCCGTGGGAGCACGCGAACGCGATC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 CAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACGCCGCCGAGATGAACGAGACC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGACACTGCTGCTGCTGAGATGAACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 gradadridararcadaaarcrirdacriccaddadcrirdccracadacccccrc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 GAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCACCGGCTCGTTCCCCGTCTCCCGGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating aplastic anemia, involves culturing the stem cells with growth medium comprising chimera protein, and harvesting the cultured stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Braford-Goldberg SR, Caparon MH, Easton AM;
Olins PO, Paik K, Thomas JW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 176; 202pp; English.
                                                                                                  92US-00981044.
93WO-US011197.
94US-00192325.
95WO-US001185.
95US-00411795.
95US-00411795.
                                                                   26-FEB-2002; 2002US-00083446
                                                                                                                                                                                                                                                          ABRAMS M A.
BRAFORD-GOLDBERG S
CAPARON M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.2
Matches 322; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Abrams MA,
Mckearn JP,
                                                                                                                                                                                                                                                                                                            EASTON A M.
KLEIN B K.
MCKEARN J P.
OLINS P O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-096775/10.
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THOMAS J W.
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US2003185790-A1.
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06-JUN-1995;
09-DEC-1996;
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22-NOV-1993;
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                                 02-OCT-2003
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Klein BK,
                                                                                                                                                                                                                                                                                                                                          (MCKE/)
(OLIN/)
(PAIK/)
(THOM/)
                                                                                                                                                                                                                                                                                            (CAPA/)
(EAST/)
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(BRAF/)
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AN A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human controlled in the r1-R1 or R1-R1, where R1 is a mutant or variant of human concluding cytokine, 1 graphokine, interleukin, haematopoietic growth factor cor IL-3 variant, and L is a linker. Genetic sequences are described in cor IL-3 variant, and specifically claimed examples are shown in AAR79398-R79335 and AAR79342-R79345. The fusion protein is made by recombinant DNA techniques. Specifically claimed examples of DNA sequences (including the present sequence) which encode these proteins care shown in AAQ7167-Q92204 and AAQ97222-Q97220. The fusion protein is used to increase hematopoietic cell production. It is also useful as an tithodies useful in immunoassays and immunotherapy. Antagonists are used to block the growth of certain cancer cells and in treatment of asthma. The fusion protein can also be used to stimulate bone marrow and blood cell activation and growth in vitro before infusion; and to treat diseases characterised by decreased levels of myeloid, erythroid, Indiseases characterised by decreased levels of myeloid, erythroid, Indiseases characterised by decreased levels of myeloid, erythroid, Indiseases characterised by decreased levels of myeloid, erythroid, Indisease the usual activity of both its component proteins, but may
GAGCTGTACAAGCAGGGCCTGCGGGGCCTCCACCAAGCTCAAGGGCCCCTTGACCATG 240
                                                                                                      351
                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                               ATCATCACCTTCGAGGGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine; mutant; mutein; fusion protein; linker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion proteins comprising a human interleukin-3 variant, a linker and interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
                                                                                                      292 ATGGCGTCCCACTACAAGCAGCACTGCCCACCGGACCCCCGGAGACCTCCTGCGCCCACG
                                                                                                                                                                             301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCTTT
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Thomas JW;
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Olins PO, Paik K,
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                                                                                                                  51 CATGGCGCCAGCGCCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGAT 110
                                                                                                                                                                                                                                                                                                                                                                                                                351 GATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCGTT 410
                                                                                                                                     618 GGAGCTGTACAAGCAGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCAT 677
                                                                                                                                                                                                                                                                                                                                                                          619 GATGGCCAGCCACTACAAGCAGCACTGCCCTCCAAACTTCCTGTGCAACCCA 737
                                                                                                                                                                                                                                                                                                                                                                                                                                   have increased synergistic activity and reduced undesired side effects
                                                                                        0; Gaps
                                                       Query Match 61.4%; Score 281; DB 2; Length 822; Best Local Similarity 83.1%; Pred. No. 4.8e-42; Matches 320; Conservative 0; Mismatches 65; Indels
                             Seguence 822 BP; 222 A; 244 C; 180 G; 176 T; 0 U; 0 Other;
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Sequence 17, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl

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Perfect score:

Sequence:

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Scoring table:

Database

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1 CGGCCCGGGATGCACCACCACCACCACTCCTCCGGCATCGAGGCCCGCATGGCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10723083
; Publication No. US200500502A1
; GENERAL INFORMATION:
    APPLICANT: Altocaar, Illimar
    APPLICANT: Bardana, Ravinder
    APPLICANT: Dudani, Aai
    APPLICANT: Tackaberry, Billean
    TITLE OF INVENTION: Production of GM-CSF in Plants
    FILE REFERENCE: O8-898901US
    CURRENT APPLICATION NUMBER: US/10/723,083
    CURRENT FILING DATE: 2003-11-26
    PRIOR FILING DATE: 2002-11-26
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: Patentin version 3.1
    SEQ ID NO 1
    LENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 458; DB 19;
Best Local Similarity 100.0%; Pred. No. 7.2e-110;
Matches 458; Conservative 0; Mismatches 0;
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US-10-901-417-16

US-10-901-417-16

US-10-14-090-509

US-10-14-090-14

US-10-411-026-17

US-10-411-026-17

US-10-411-026-17

US-10-410-997-17

US-10-410-997-17

US-10-410-997-17

US-10-410-997-17

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US-10-410-991-17

US-10-410-991-17

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US-10-410-980-17

US-10-410-980-19

US-10-429-980-32

US-10-429-980-32

US-10-429-980-32

US-10-429-980-32

US-10-429-980-30

US-10-429-980-30

US-10-45-024-8

US-10-486-98-34

US-10-486-98-34

US-10-278-698-34

US-10-278-698-34

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US-10-278-698-34

US-10-278-611-3

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US-10-48-98-31A-187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (10)..(438); OTHER INFORMATION:
US-10-723-083-1
    FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-10-723-083-1
    TYPE: DNA
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                                                                                                      March 11, 2005, 16:42:11; Search time 453 Seconds (without alignments) 6014.183 Million cell updates/sec
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Sequence 3,
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                                                                                                                                                                                                 1 cggcccgggatgcaccacca.....gctagcgtcgacgcatgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_MEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-723-083-3
US-10-188-056-33
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US-10-083-446-55
US-10-083-446-69
US-10-083-446-69
US-10-083-446-69
US-10-083-446-99
US-10-69-346-9
US-10-69-346-19
US-10-69-346-19
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                                                                                                                                                                                                                                                                        5537552 segs, 2974263231 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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458 318.6 312.6 311 283.6 283

Result

281 277 276.8 276.8

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309
  121 CTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTGATATCAGAA 180
                                                                                                                                                          CAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGC 369
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                                                              ATGTTTGACCTCCAGGAGCGGACTTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGC
                                                                                                                     CTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAG
                                                                                                                                                                                                                                                                                                                  361 TTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTC
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APPLICANT: Lai, Wan-Ching
APPLICANT: Chu, Yong Liang
APPLICANT: Chu, Yong Liang
APPLICANT: Chu, Yong Liang
APPLICANT: Chu, Frank Q.
TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
FILE REFERENCE: 3781-004-27
CURRENT APPLICATION NUMBER: US/10/188,056
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 312.6; DB 1
Pred. No. 5.7e-72;
0; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/10188056
Publication No. US20040009934A1
GENERAL INFORMATION:
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82.8%;
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Best Local Similarity 82.8
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                        430 CAGGAGTGA 438
                                                                                                                                                                                                                                                                                                                                                                                             421 CAGGAGTGA 429
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CORGANISM: Homo sapiens
US-10-188-056-31
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LENGTH: 435
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                                                            61 GCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGACCACGTGAACGCGATCCAGGAGGCC 120
                                                                                                                   CGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGGACCGTGGAGGTG 180
                                                                                                                                                                                              ATCTCCGAGATGTTCGGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTAC 240
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CGGCCCGGGATGCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCA 60
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Pred. No. 1.6e-73;
0; Mismatches 69; Indels
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APPLICANT: Sardana, Ravinder
APPLICANT: Sardana, Ravinder
APPLICANT: Ganz, Peter
APPLICANT: Ganz, Peter
APPLICANT: Tackaberry, Eilleen
TITLE OF INVENTION: Production of GM-CSF in Plants
FILE REPERENCE: 08-898901US
CURRENT FILING DATE: 2003-11-26
PRIOR PILING DATE: 2003-11-26
PRIOR PILING DATE: 2003-11-26
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 GAGCCGGTGCAGGAGTGAGCTAGCGTCGACGCATGCCG 458
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Best Local Similarity 83.9%;
Matches 360; Conservative
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; OTHER INFORMATION:
US-10-723-083-3
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TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB.1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. CALISCOPHER BAUER
REGISTRATION NUMBER: C-2790/6
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TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                           Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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:ULE TYPE: DNA (genomic)
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LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                         Thomas, John W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
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                                                     GCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGACTGCTGGGGAGCCCG 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGCCCGCATGGCGCCAGCGCGCA
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Li, Frank Q.
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; CURRENT APPLICATION NUMBER: US/10/188,056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.9%; Score 311; DB 17; Length 435; 82.6%; Pred. No. 1.5e-71; tive 0; Mismatches 75; Indels
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US-10-083-446-55
Sequence 55, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.6
Matches 356; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180
                                                                                                                                                                                                61 caggadgecedegererecreaacergagragagacacacacacrecreagardaardaaaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360
                                                                                                                                                   CAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGAGAACGAGACC 171
                                                                                                                                                                                                                                                                                                                                              232 GAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGCCCGCTCACCATG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                          292 ATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAG 351
                                                                                                   1 ATGGCACCGGCTCGTTCCCCGGTCTCACCCAGCCGTGGGACACACGTGAATGCCATC
                                                                                                                                                                                                                                                                                                                                                                       181 GAGCTGTACAAGCAGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ATGGCCAGCCACTACAAGCACTCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG
       0; Gaps
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ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
       65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                      52 ATGCCCCAGCCCCAGCCCCGAGCCCGTCCACCCAGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR DATE: 26-Feb-2002
CLASSIFICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION SATE: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/46,872
FILING DATE: 06-JUN-1995
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 GACTGCTGGGAGCCGGTGCAGGAGTGA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GACTGCTGGGAGCCAGTCCAGGAGTGA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caparon, Maire H. Baston, Alan M. Kılein, Barbara K. McKearn, John P. Olins, Peter O. Paik, Kumman Thomas, John W.
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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Braford-Goldberg,
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COMPUTER READABLE FORM:
    Matches 322; Conservative
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TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACCCCTCCAACCCCGGAA 675
                                                                                                        334 ACCICCIGCCCACCCAGAICAICAICTICGAGAGCTICAAGGAGAACCICAAGGACTIC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
COrporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.8%; Score 283; DB 16; Length 402; 83.2%; Pred. No. 3e-64;
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COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002

CLASSIFICATION: UNMBER: 08/762,27

PRIOR APPLICATION NUMBER: 08/762,227

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/46,872

FILING DATE: 06-UN-1995

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42-7305

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
                                                                                                                                                                       394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
                                                                                                                                                                                                                    736 crectrercarcecertreachecheeaaccaerceagaa 777
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Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 176: US-10-083-446-176
                                                                                                                                                                                                                                                                                                                                         Sequence 176, Application US/10083446 Publication No. US20030185790A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: St. Louis
STATE: Missouri
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Best Local Similarity
                                                                                                                                                                                                                                                                                            RESULT 6
US-10-083-446-176
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111 CCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACGCCCCCCGAGATGAACGAGAC 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    639 AGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          699 GGAGCTGTACAAGCAGGCCTGCGGGGCAGCTCACCAAGGCCCCTTGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 careceacececercerececerececereraceasecereseaacacereaarecear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 CGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 281; DB 16;
Pred. No. 9.7e-64;
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION AUTORN:
APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/195
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
61.4%; Score 281; DB
Best Local Similarity 83.1%; Pred. No. 9.7e
Matches 320; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGIERATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
                                                                    JTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-10-609-346-9
; Sequence 9, Application US/10609346
; Publication No. US20040063635A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 903 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 66
SEQUENCE CHARACTERISTICS
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                                                                         COMPU
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TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 CATGGCGCCAGCGCGCAGCCCGAGCCCGTCCAGCCGTGGGAGCACGTGAACGCGAT 110
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Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 281; DB 16; Length 822;
Pred. No. 9.7e-64;
0; Mismatches 65; Indels
                    NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sarah R.
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-083-446-69
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Braford-Goldberg, S.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                 TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/10083446
Publication No. US20030185790A1
                                                                                                                                                                                                               LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.1%;
Matches 320; Conservative
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US-10-083-446-66
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0
                                                                  Length 448;
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                                         Score 276.8; DB 17; Leasure. Pred. No. 1.2e-62;
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Pred. No. 1.2e-62;
0; Mismatches 97; Indels
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| Sequence 20, Application US/10447315 |
| Publication No. US20040071687Al |
| GENERAL INFORMATION: |
| APPLICANT: Rafii, Shahin |
| APPLICANT: Heisaig, Beate |
| APPLICANT: Heisaig, Roichi |
| APPLICANT: Heisaig, Roichi |
| APPLICANT: Cornell Research Foundation, Inc. |
| TITLE OF INVENTION: Adult Stem Cell Recruitment |
| FILE REFERENCE: 1676.006US1 |
| CURRENT FILING DATE: 2003-05-28 |
| PRIOR FILING DATE: 2002-05-28 |
| NUMBER OF SEQ ID NOS: 28 |
| SEQ ID NO 20 |
| LENGTH: 781
                                                                                                                             0; Mismatches
                                                                  60.48;
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Best Local Similarity 77.5
Matches 335; Conservative
                                                              Query Match 60.4
Best Local Similarity 77.5
Matches 335; Conservative
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US-10-609-346-19
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                    APPLICANT: Yu, Zailin
APPLICANT: Yu, Zailin
APPLICANT: Yu, Zailin
APPLICANT: Fu, Yan
APPLICANT: Fu, Yan
TITLE OF INVENTION: EFFECTS
FILE REFERENCE: ZYU-0603
CURRENT APPLICATION NUMBER: US/10/609,346
CURRENT APPLICATION NUMBER: US 60/392,948
PRIOR APPLICATION NUMBER: US 60/392,948
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 9
LENGTH: 2211
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US-10-609-346-19
Squance 19, Application US/10609346
Fublication No. US20040063635A1
GENERAL INFORMATION:
APPLICANT: Yu, Zailin
FITLE OF INVENTION: EFFECTS
FITLE OF INVENTION: EFFECTS
FITLE OF INVENTION: WHERE: US/10/609,346
CURRENT APPLICATION NUMBER: US/10/609,346
FRICH APPLICATION NUMBER: US/2002-06-26
PRIOR PRIOR PELICATION NUMBER: US/2002-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1943 CAGTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCC 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2123 AGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCT 2182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGTGGAGGTGATCTCCGAGATGTTCGATCTCCCAGGAGCCGACCTGCCTCCAGACCCGCC 229
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Pred. No. 1.1e-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Seguence
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.0%;
Matches 319; Conservative
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Best Local Similarity
GENERAL INFORMATION:
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248 GCCTCCGCGGCAGCCTCACCAAGGTCAAGGGCCCGCTCACCATGATGGGGTCCCACTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fish, Paul. V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIncosh, Fraser S
APPLICANT: McIncosh, Praser S
APPLICANT: Occleston, Nicholas L
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/10/10/11/985
PRIOR APPLICATION NUMBER: US/10/11/985
PRIOR FILING DATE: 2002-04-25
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                             428 TGCAGGAGTGAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 TCCAGGAGTGAG 468
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US-10-901-417-16
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                                   TCCTCAACCTCTCCCGCGACACCGCCGCGAGATGAACGAGACGTGGAGGTGATCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Davies, Michael J
APPLICANT: Davies, Michael J
APPLICANT: Bayles, Michael J
APPLICANT: Huggins, Jonathan P
APPLICANT: Huggins, Jonathan P
APPLICANT: Mointosh, Fraser S
APPLICANT: Mointosh, Fraser S
APPLICANT: Mointosh, Richolas L
TILE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/09/726,295
PRIOR APPLICATION NUMBER: US/09/726,295
PRIOR APPLICATION NUMBER: GB 9930768.8
PRIOR FILING DATE: 1999-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 16, Application US/10131985; Publication No. US20030199440A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Patentin Ver. 2.1
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 16
LENGTH: 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-131-985-16
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US-10-131-985-16
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                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                      STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/826,025
FILING DATE: 04-Apr-2001
CLASSIFICATION NUMBER: US/09/826,025
FILING DATE: 04-Apr-2001
CLASSIFICATION NUMBER: 08/838,702
FILING DATE: 4Uhknown>
APPLICATION NUMBER: 08/838,702
FILING DATE: 4Uhknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

BESCRIFTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-826-025-8
ADDRESSEE: Medlen & Carroll,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 435 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS
                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 77.5
Matches 334; Conservative
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                                                                                                                                                                                                                                                                                                                Sequence 509, Application US/10044090
FUNDICATION NO. US20020137081A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION: GENES US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 509
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                            GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAAGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20020137081A1 370489.47 US-10-044-090-509
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TITLE OF INVENTION: Combination Immunogene Therapy
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTGGGAGCCGGTGCAGGAGTGAG 439
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Patent No. US20020162123A1
GENERAL INFORMATION:
                                                                                                                                 439
                                                                                                                                                                                       TCCAGGAGTGAG 468
                                                                                                                                 TGCAGGAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                      RESULT 14
US-10-044-090-509
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US-09-826-025-8
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Search completed: March 11, 2005, 18:28:48 Job time : 457 secs ABX00086 ADJ14388

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AAQ97208 AAA03771

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RESULT 1
us-10-723-083-2.rng
                                                                                                                         Command line parameters:
-MODBL=frame+ p2n.model.-DEV=xlh
-Q=/Cgn2_1/USPTO_spool/US10723083/runat_08032005_131715_10414/app_query.fasta_1.327
-Q=/Cgn2_1/USPTO_spool/US10723083/runat_08032005_131715_10414/app_query.fasta_1.327
-DB=N Geneseq_16Dec04 -QFWT=fastap -SUFFTX=rng -MINNATCH=0.1 -LOOFCL=0
-LOOPEXT=0 -UWITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORES=pct -THR MAX=100 -THR MIN-0 -ALIGNS=15
-MODB=LOCAL -OUTFMT=pto -NOFM=axt -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10723083_@CGN 1 1 644_@runat_08032005_131715_10414 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPOR=10 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOR=10 - KGAPOP=6
-FGAPOXT=7 -YGAPOP=10 -YGAPOXT=0.5 -FGAPOP=6
                                                                                                                                                                                                    March 11, 2005, 17:24:26 ; Search time 473 Seconds
    (without alignments)
    1777.174 Million cell updates/sec
                                                                                                                                                                                                                                                                                     765
1 MHHHHHHSGIEGRMAPARS......ENLKDFLLVIPFDCWEPVQE
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                                                                                                        version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                                                                       nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                      4390206 segs, 2959870667 residues
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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Fgapop 6.0 ,
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Aat34400 Granulocy
Aba96672 Human gra
Aag97208 PMON13012
Aaa03771 Human G-C
Abx00086 Human int
Adi14388 DNA relat
Aan90214 Synthetic
Aan90233 Synthetic
Aag97183 PMON13035
Aaa03737 Human int
Adj14281 DNA relat
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Aag14278 DNA relat
Aac16718 Human int
Adj14278 DNA relat
Aax288268 Granulocy
Aat399 Granulocy
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Aat399 Granulocy
Aat36194 Self-coal
Aav83189 Granulocy
Aan81320 Sequence
Adf15808 Human alb
Adf15808 Human alb
Adf15715 Human alb
Adf15715 Human alb
Adf15719 Human alb
Adf157089 Human GMAd120789 Human GMAd14089 Human GMAd167022 Human GRAd116729 Human Gra
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ABX00023 ADJ14278 AAZ50587

Perfect score:

Sequence:

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ABX00026 ADJ14281 AAQ97180 AAA03734

AA097183 AAA03737

AAN90274

ADL16719
AAZ88268
AAT34399
AAN81320
ADJ36194
AAV83189

AAA64392 ADF15808

ADF15714 ADF15807

ADF15715 ACC78877 AD120788 AD120789 ADN49689 ADQ76022 ADQ76023 AAN81321 ADL16729

ALIGNMENTS

ADS88046 ADJ36238

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Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine; mutant; mutein; fusion protein; linker; 88.
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                                                                                                                                                                                                             Caparon MH,
Thomas JW;
                                                                                                                                                                                                             Braford-Goldberg SR,
Olins PO, Paik K,
                                                         pMON13022 DNA encoding IL-3 fusion protein.
       B.
                                                                                                                                                                             94US-00192325.
                                                                                                                                                            95WO-US001185
       AAQ97169 standard; DNA; 777
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Mckearn JP,
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BK,
                       AAQ97169;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:*

Database :

SUMMARIES

Aaq97169 PMON13022 Aaa03723 Human int Abx00012 Human int Adj14267 DNA relat Aat72724 p53-GM-CS

AAQ97169 AAA03723 ABX00012 ADJ14267 AAT72724

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89.2 89.2 89.2 89.2 88.8

682 682 682 682 679

4 0 M 4 G

9 17 2

Description

a

Query Match Length DB

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Result Š

WPI; 1995-283774/37.

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A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human interleukin-3 (h1L-3), R2 is a second colony stimulating factor (CSF) including cytokine, lymphokine, interleukin, haematopoietic growth factor or IL-3 variant, and L is a linker. Generic sequences are described in AAW03235 - AAW03242, and specifically claimed examples are shown in ARY9298-R79335 and AAR7924-R79345. The fusion protein is made by recombinant DNA techniques. Specifically claimed examples of DNA sequences (including the present sequence) which encode these proteins are shown in AAQ9716-T09724 and AAQ9722-Q9727. The fusion protein is used to increase haematopoietic cell production. It is also useful as an III-3 antagonist or as a discrete antigenic fragment for production of antibodies useful in immunoassays and immunotherapy. Antagonists are used to block the growth of certain cancer cells and in treatment of asthma. The fusion protein can also be used to stimulate bone marrow and blood cell activation and growth in vitro before infusion; and to treat lymphoid and/or megakaryocyte cells of myeloid, erythroid, lymphoid and/or megakaryocyte cells of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic system. The proteins, but may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein has the usual activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects
                                                                                        Fusion proteins comprising a human interleukin-3 variant, a linker e interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
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                                                                                                                                                                                                               Claim 22; Page 158-159; 447pp; English.
                               P-PSDB; AAR79317
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ID AAA03723 standard; DNA; 777 BP.
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Query Match:
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Human interleukin-3 mutant containing fusion protein DNA SEQ ID NO:55
                                       Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine; colony stimulating factor; haematopoietic growth factor; lymphokine; fusion protein; haematopoietic disorder; infection; cancer; radiation therapy; chemotherapy; bone marrow suppressive drug; bone marrow activation; blood cell activation; blood transplant; ds.
                 (first entry)
                 19-MAY-2000
     AAA03723;
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sapiens.

Ношо

Synthetic.

US6022535-A

94US-00192325. 95WO-US001185. 95US-00411795. 95US-00469318, (SEAR) SEARLE & CO G D. Abrams MA, 06-JUN-1995; 06-APR-1995; 04-FEB-1994; 08-FEB-2000 SC,

mutated other Treating hematopoietic disorders with fusion proteins comprising interleukin-3 fused with secondary colony stimulating factors or interleukin-3 variants. Easton AM, Caparon MH; Braford-Goldberg SR, skearn JP, Olins PO, Mckearn JP, WPI; 2000-160368/14. Paik K, Thomas JW,

Example 27; Col 135-136; 276pp; English.

fusion proteins comprising recombinant, mutated human interleukin-3 (hilltustion proteins comprising recombinant, mutated human interleukin-3 (hillSimulating factors (CSFs) (e.g. cytokines, interleukin)
and/or haematopoietic colony stimulating factors) or other interleukinand/or haematopoietic colony stimulating factors) or other interleukincontraints with or without a linker. The methods may be used in vivo to
treat haematopoietic disorders resulting from bacterial, viral and fungal
infections, cancer radiation therapy, chemotherapy or bone marrow
suppressive drugs. They may also be used in vitro to stimulate bone
constrow and blood cell activation and growth prior to infusion of the bone
constrow and blood cell activation and growth prior to infusion of the bone
constrow and blood transplants into patients IL-3 is a haematopoietic
constrow and blood defferentiation of haematopoietic cells. The fusion
concludes are characterised by possessing the usual activity of both of
their constituent peptides and further by having a biological or
concluded activity greater than the additive function of the IL-3 or
second CSF alone (i.e. the peptides act synergistically). Their activity
concluded the average oundesirable side effects associated with IL
constituent payone reduce undesirable side effects associated with IL
constituent by average the mutations they comprise. The Methods have been developed for treating haematopoietic disorders with represent sequences the present invention AY53130 to AAY53226, and AAA03721 to AAA03782 in the exemplification of the present inventio AAY53130

Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

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777
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      Length:
Matches:
Conservative:
Mismatches:
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       1.38e-67
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(1-777)US-10-723-083-2 (1-142) x AAA03723 us-10-723-083-2.rng

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Disclosure; Col 161-164; 203pp; English
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                                                                                                                                                              LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
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                                                                                                                                                                                                                                                                                                                                                                                               Haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; ds; GCSF; G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand; human growth hormone; B-cell growth factor; leukaemia; flt3 ligand; human growth hormone factor; eosinophil differentiation factor; stem cell differentiation factor; eosinophil differentiation factor; stem cell factor; SCF; cyclic neutrophia; aplastic anaemia; rhrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome; systemic lupus erythematosus; SLE; myelodysplastic syndrome; myelofibrosis; Interleukin-3; IL-3; stem cell.
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           TCTGGCGCGCGCTCCAA.CATGGCACCGGCTCGTTCCCCGTCTACCCAGCCGTGG
                                                     GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT
                                                                                                                                                                                                                      ACTICCTGTGCGAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC
                                                                                             GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT
                                                                                                                          CysleuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu
                                                                                                                                      SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp
                                         GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla
                                                                                 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr
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Thomas JW;
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Mckearn JP,
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04-FEB-1994;
04-FEB-1995;
06-APR-1995;
06-JUN-1995;
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The invention relates to ex vivo expansion of stem cells, comprises culturing stem cells with a growth medium comprising a chimaera protein, and harvesting the cultured stem cells. The chimaera is based on a mutated human interleukin-3 (IL 3) sequence coupled to a haematopoietic factor (e.g. GW-CSF (colony stimulating factor), CSF-1, G-CSF, G-CSFS-1, To-chill ligand TPO, MODF, erythropoietin, IL-13, IL-15, IL-15, CF12 ligand, human growth hormone, B-Cell growth factor, B-Cell Gfferentiation factor, eosinophil differentiation factor and stem cell cator (SCF) via a peptide linker. The formula for the chimaera is given in the specification. Also included is a method for enhancing the comprising; (a) removing stem cells from a patient or donor; (b) culturing the stem cells with a growth medium comprising the transduced comprising; (a) removing stem cells from a patient or donor; (b) culturing the stem cells with a growth medium comprising the transduced cells. The method is also useful for treating a patient conflex a heartopoietic disorder. The expanded haematopoietic cells by a cherrologous gene. The method is also useful for treating a patient coll avoing a haematopoietic disorder. The expanded haematopoietic cells are also useful in the treatment of cyclic neutropenia, aplastic and coll and myelofibrosis. The present sequence is an IL-3 mutant associated DNA sequence. Note: The present sequence is an IL-3 mutant associated DNA sequence. Note: The present sequence is an IL-3 mutant associated DNA cepture of the present sequence is an interpretation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerThrGlnProTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AlaGluMetAsnGluThrValGluVallleSerGluMetPheAspLeuGlnGluProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676 ACTICCIGIGGAACCCAGAITAICACCITIGAAAGITITCAAAGAGAACCIGAAGGACTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;
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89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
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                                                                            SerGly11eGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp
                                                                                                                                                      29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuLeuVallleProPheAspCysTrpGluProValGlnGlu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  736 CIGCTIGITCATCCCCTTTGACTGCTGGGAGGCCAGTCCAGGAG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product= "p53-GM-CSF fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p53-GM-CSF immunostimulant fusion protein DNA.
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/product= "Ser-Arg linker"
Gaps:
                                      US-10-723-083-2 (1-142) x ADJ14267 (1-777)
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188, .1193
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                                                                                          stem cell; antianaemic; immunostimulant; immunomodulator; antiinflammatory; dermatological; immunosuppressive; cytostatic; antiinflammatory; hæmopoietic disorder; gene therapy; myeloid; erythroid; lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia; chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia; myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating aplastic anemia, involves culturing the stem cells with growth medium comprising chimera protein, and harvesting the cultured stem cells.
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                                                        SEQ ID
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                                                      DNA related to human interleukin-3 (IL-3) mutant protein
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Olins PO, Paik K, Thomas JW;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                   92US-009B1044.
93WO-US011197.
94US-00192325.
95WO-US0011B5.
95US-00446872.
96US-00762227.
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89.15%
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BRAFORD-GOLDBERG S I
CAPARON M H.
                  (first entry)
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Mckearn JP,
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KLEIN B K.
MCKEARN J P.
OLINS P O.
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C.
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                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                 26-FEB-2002;
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02-FEB-1995;
06-APR-1995;
                  20-MAY-2004
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22-NOV-1993
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09-DEC-1996
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Klein BK,
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(ABRA/) (BRAF/) (CAPA/) (EAST/) (KLEI/) (MCKE/)

BAUE/)

(PAIK/) (THOM/)

Query Match:

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JP08173185-A.
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1485 GCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTC 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1245 AATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGCTGAGATG 1304
                                                                                                           A nucleic acid molecule (AAT72724) codes for a fusion protein (AAM19763) comprising human p53 tumour suppressor protein and granulocyte-macrophage colony stimulating factor (GM-CSF). It was prepd. by PCR amplification of p53 cDNA GM-CSF CDNA sequences (the GM-CSF antiense primer including a hexahistidine tag sequence) and their fusion via a Xbal linker. Fusion expression vectors can be used to transfect mammalian and insect cells. The p53-GM-CSF fusion protein is used to generate anti-p53 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen-presenting cells exposed to the fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVal 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGln 71
                                   Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response in a vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1425 TTGACCATGATGGCCAGCCACTACAAACAGCACTGCCCTCCAACCCCGGAAACTTCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GM-CSF; granulocyte macrophage colony-stimulating factor; expression; construct; stable; production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Granulocyte macrophage colony-stimulating factor coding sequence
                                                                                                                                                                                                                                                    Sequence 1610 BP; 383 A; 508 C; 407 G; 312 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                    4000
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Matches:
Conservative:
Mismatches:
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                                                                                      Example 7; Fig 11; 45pp; English
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97.71%
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(first entry)
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Percent Similarity:
Best Local Similarity:
           P-PSDB; AAW19763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
11-FEB-1997
                                                 response subject.
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                                                                                                                                                                                                                            protein
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DB:
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AAT34400
ID AAT3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                            The present sequence encodes human granulocyte macrophage colony-stimulating factor (hGM-CSF; n = 101, 11e). A series of oligonucleotides were synthesised and ligated together to form a stable expression construct. The technique is used for the efficient prodn. of a glycoprotein with hGM-CSF activity. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 MetAlaSerHisTyrLysGlnHisCysProFroThrProGluThrSerCysAlaThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ATGGCTAGCCATTACAAACAGCATTGTCCGCCGACTCCGGAAACTTCTTGTGCTACTACAG
                                                                                                                                                                                                          - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 MetalaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGCACCAGCTCGATCACCGTCCCCGTCCAACCATGGGAACATGTTAACGCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAGGAAGCTCGTCGTCGTCGTGAACCTGTCTCGTGATACTGCTGCTGAAATGAACGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 ValGluValileSerGluMetPheAspLeuGluGluProThrCysLeuGlnThrArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet
                                                                                                                                                                                                        Prodn. of human granulocyte macrophage colony-stimulating factor culturing E. coli transformed with human GM-CSF DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 0 U; 0 Other;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                      Claim 1; Page 2; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA96672 standard; cDNA; 384 BP
95JP-00263370
                                        87JP-00106148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5e-67
678.00
100.00%
100.00%
88.63%
                                                                               (AMGE-) AMGEN INC.
(KIRI ) KIRIN BREWERY
                                                                                                                                           WPI; 1996-365600/37...
N-PSDB; AAW00103.
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Best Local Similarity:
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The invention relates to the recombinant production of human granulocyte macrophage-colony stimulating factor (hGW-CSF). NcoI and BamHI restriction sites were inserted into hGW-CSF CDNA (ABA96672) via PCR using primers ABA96670-ABA96671, prior to cleavage with these enzymes insertion into the pET-11d vector downstream of the T7/lac promoter to GDCm the plasmid pT7GMCSF. pT7GMCSF was transformed into Escherichia coli sequence represents hGM-CSF cDNA
                                                                                                                                                                        Human granulocyte macrophage-colony stimulating factor (hGM-CSF) cDNA.
                                                                                                                                                                                                                                                          Human; GM-CSF; granulocyte macrophage-colony stimulating factor; recombinant production; Escherichia coli; pET-11d vector; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim HS
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                                                                                  (first entry)
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                                                                                      23-APR-2002
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ABA96672;
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Sequence 384 BP; 93 A; 125 C; 97 G; 69 T; 0 U; 0 Other;

Scores: 1.5e-67 Length: 384 678.00 Matches: 128 milarity: 100.00\$ Conservative: 0 Similarity: 100.00\$ Mismatches: 0 h: 88.63\$ Indels: 0 2 Gaps: 0	3-2 (1-142) x ABA96672 (1-384)	S MetalaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34	1 ATGGCACCCGCCCGCTCGCCCAGCCCCAGCACGCACCCCTGGAGCATGTCATC 60	GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaAlaGluMetAsnGluThr 54	CAGGAGGCCCGGCGTCTCCTGAACCTGAGAGACACTGCTGCTGGTGAATGAA	S ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74		5 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94	GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGGCCCCCTTGACGGCCCCTTGACGATGAAGCTCAAGGGCCCCTTGACCATG 240	S MetalaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114		5 IlelleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPhe 134	ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTT 360
went S No.: nt Sim	US-10-723-083-2	15	Г	35	61	55	121	75	181	95	241	115	301
Aligna Pred. Score: Percer Best I Query DB:	us-	ò	Q	ò	g	à	đ	ò	g	ò	g	ò	g,

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Interleukin, hIL-3; CSF; colony stimulating factor; cytokine; lymphokine; mutant; mutein; fusion protein; linker; ss.
                                                                                                                                                                                                                                                                                               Fusion proteins comprising a human interleukin-3 variant, a linker and interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
                                                                                                                                                                                                                                                Easton AM;
                                                                                                                                                                                                                                               Caparon MH,
Thomas JW;
                                                                                                                                                                                                                                               Braford-Goldberg SR,
Olins PO, Paik K,
135 AspCysTrpGluProValGlnGlu 142
        361 GACTGCTGGGAGCCAGTCCAGGAG 384
                                                                                                                                                                                                95WO-US001185.
                                                                                                                                                                                                               94US-00192325.
                                               AAQ97208 standard; DNA; 402
                                                                              25-AUG-1999 (first entry)
                                                                                                                                                                                                                              (SEAR ) SEARLE & CO G D.
                                                                                              pMON13012 DNA sequence.
                                                                                                                                                                                                                                                Abrams MA,
Mckearn JP,
                                                                                                                                                                                                                                                                      WPI; 1995-283774/37.
P-PSDB; AAR79338.
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                               04-FEB-1994;
                                                                                                                                                                                               02-FEB-1995;
                                                                                                                                                                W09521254-A1
                                                                                                                                                                                10-AUG-1995.
                                                                                                                                                                                                                                               Bauer CS,
Klein BK,
                                                                                                                                       Synthetic.
                                                               AAQ97208;
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ARA new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human interestion interleukin-3 (InL-3), R2 is a second colony stimulating factor (CSF) including cytckine, lymphokine, interleukin, haematopoietic growth factor or IL-3 variant, and L is a linker. Generic sequences are described in AAM03223. AAM03232, and specifically claimed examples are shown in AAR03298-R79345. The fusion protein is made by recombinant DNA techniques. Specifically claimed examples of DNA recombinant DNA techniques. Specifically claimed examples of DNA combinant DNA techniques. Specifically claimed examples of DNA combinant DNA techniques. Specifically are shown in AAR097167-067-067-204 and AAR097222-097227. The fusion protein is used to increase heematopoietic call production. It is also useful as an IL-3 antagonist or as a discrete artigenic fragment for production of antibodies useful in immunosassays and immunotherapy. Antagonists are used to block the growth of certain cancer cells and in treatment of asthma. The fusion protein can also be used to estimilate bone marrow and blood cell activation and growth in vitro before infusion; and to treat diseases characterised by decreased to hemmatopoietic system. The protein has the usual activity of both its commonsant rarefering but may have interesting anneary and and commonsant rarefering but has additional and commonsant rarefering both its component proteins, but may have increased synergistic activity and reduced undesired side effects

Example 19; Page 183; 447pp; English.

G; 78 T; 0 U; 0 Other; Sequence 402 BP; 99 A; 124 C; 101

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       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
        1.59e-67
               678.00
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88.63%
                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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CC fusion proteins comprising recombinant, mutated human interleukin-3 (hilt-studing proteins comprising recombinant, mutated human interleukin-3 (hilt-stimulating comprising recombinant, mutated human interleukin-3 (stimulating factors (GSFs) (e.g. cytokines, lymphokines, interleukin-3 cand/or haemacopoietic colony stimulating factors) or other interleukin-3 card/or haemacopoietic colony stimulating factors) or other interleukin-3 card/or haemacopoietic colony stimulating factors) or other interleukin-3 card/or haemacopoietic calony stimulating factors bone marrow and blood call activation in therapy, chemotherapy or bone marrow and blood cranaphants into patients. IL-3 is a haemacopoietic growth factor which has the property of being and to promote the currowth factor which has the property of being and activity of both of their constituent peptides and further by having a biological or physiological activity greater than the additive function of the IL-3 or physiological activity greater than the additive function of the IL-3 or comprise. The evend CSF alone (i.e. the peptides act synergistically). Their activity may also be further enhanced by the mutations they comprise. The contituences and further by having a biological or contains may further reduce undesirable side effects associated with IL-3. Are are altitudes and AAA01721 to AAA03121 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ATTATCACCTTTGAAAGTTTCAAAGACAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention
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Matches:
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100.00%
88.63%
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ID ABX0
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AC ABX0
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DT 18-D
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KW Haem
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                                                                                                                                                                                                                                             MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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                                                                                 MetAlaproAlaArgSerProSerTroSerThrGlnProTrpGluHisValAsnAlalle
                                                                                                                     1 ATGGCACCGGCTCCTTCCCCCGTCTCCCCGCCGTGGGGAACACGTGAATGCCATC
                                                                                                                                                                                        35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr
                                                                                                                                                                                                                                                                                                                                                                                                             GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine; colony stimulating factor; haematopoietic growth factor; lymphokine; fusion protein; haematopoietic disorder; infection; cancer; addation therapy; chemotherapy; bone marrow suppressive drug; bone marrow activation; blood cell activation; blood transplant; ds.
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Caparon MH;
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kearn JP, Olins PO,
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95WO-US001185.
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interleukin-3 variants.
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06-APR-1995;
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The invention relates to ex vivo expansion of stem cells, comprises culturing stem cells with a growth medium comprising a chimaera protein, and harvesting the cultured stem cells. The chimaera is based on a mutated human interleukin-3 [IL.3] sequence coupled to a haematopoietic factor (e.g. GW-CSF (colony stimulating factor), CSF-1, G-CSF, G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ex vivo expansion of stem cells, for enhancing transduction efficiency of cultured stem cells, comprises culturing stem cells in growth medium having mutant interleukin-3, and hematopoietic factor, and harvesting
G-CSF; G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Braford-Goldberg SR, Caparon MH, Easton AM, Olins PO, Paik K, Thomas JW;
                     human growth hormone; B-cell growth factor; leukaemia; B-cell differentiation factor; eosinophil differentiation factor; stem cell factor; SCF; cyclic neutropenia; aplastic anaemia; thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome; systemic lupus erythematosus; SLE; myelodysplastic syndrome; myelofibrosis; Interleukin-3; IL-3; stem cell.
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93WO-US011197.
94US-00192325.
95US-00411795.
95US-00446872.
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Mckearn JP,
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22-NOV-1993;
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06-APR-1995;
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Klein BK,
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Length:
Matches:
    1.59e-67
678.00
100.00%
100.00%
88.63%
Alignment Scores:
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Conservative: Mismatches: Indels:

Similarity:

Query Match Best Local

Percent Similarity:

Gaps:

US-10-723-083-2 (1-142) x ABX00086 (1-402)

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15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle
                1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC
                                                                    121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCGCCTG
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                                                 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr
                                                                                                   55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - SEQ ID 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell; antianaemic; immunostimulant; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA related to human interleukin-3 (IL-3) mutant protein
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BRAFORD-GOLDBERG
CAPARON M H.
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MCKEARN J P
OLINS P O.
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THOMAS J W.
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The invention relates to a novel method whereby stem cells are ex vivo expanded via culturing the stem cells with a growth medium comprising a chimera protein, followed by harvesting of the cultured stem cells. The method of the invention has antianaemic, immunostimulant, immunomodulator, antiinflammatory, dermatological, immunosuppressive, cytostetic and heuroprotective applications and may be useful to target hasmopoietic cells for gene therapy, preferably for treating patients having a haemopoietic disorder characterised by decreased levels of system. The expanded ex vivo cells may be used to treat neutropenia, aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome, aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome, myelofibrosis. The current sequence is that of a DNA related to the human interleukin-3 (IL-3) mutant protein of the invention.
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                                                                                        Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating aplastic anemia, involves culturing the stem cells with growth medium
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   Easton AM;
                                                                                                           aplastic anemia, involves culturing the stem cells with growth medicomprising chimera protein, and harvesting the cultured stem cells.
Caparon MH,
Thomas JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
 Braford-Goldberg SR,
Olins PO, Paik K,
                                                                                                                                                            Disclosure; SEQ ID NO 176; 202pp; English.
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Abrams MA,
Mckearn JP,
                                                      WPI; 2004-096775/10
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Best Local Similarity:
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Bauer SC,
Klein BK,
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An expression plasmid contg. the DNA is prepd. and used to transform E.coli. The transformant is cultured and MPGMCSF is produced into the medium. hGMCSF stimulates the granulocyte macrophage system stem cell and promotes the formation of the granulocyte macrophage. hGMCSF is used in curing leukopeania caused by radiation therapy, or chemical therapy, or in promptly propagating leukocytes after bone marrow transplantation. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human granulocyte macrophage colony stimulus factor prepn. - by forming plasmid contg. genetic information and Escherichia coli with the plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 CAGGAAGCTCGTCGTCGTGCTGAACCTGTCTCGTGATACTGCTGCTGAAATGAACGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 GTTGAAGTGATCAGCGAAATGTTCGATCTGCAGGAACCGACTTGTCTGCAAACCCCGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 GAACTGTACAAACAAGGTCTGCGTGGTTCTCTGACTAAACTGAAAGGTCCGCTGACTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet
                           Sequence (I) encoding human granulocyte macrophage colony stimulating factor (hGMCSF) with Ile at 101.
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                                                                      Leukopoenia therapy; bone marrow transplant;
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Matches:
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                                                                                                                              Location/Qualifiers
complement(1..4)
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(KIRI ) KIRIN BREWERY
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Best Local Similarity:
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194 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGGTCAAGGGCCCCTTGACCATG 253
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                                                                                                                                                                                                                                                                                             115 ileileThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPhe 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human granulocyte-macrophage colony stimulating factor - synthetic DNA includes restriction sites for cassette mutagenesis and incorporation in expression systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic DNA encoding human granulocyte colony stimulating factor (GM-CSP), see corresp. AAP90115. Has useful restriction sites for: HindIII; BspMI; NocI; BstEII; BsmI; EcoRV; BgII; ApaI; Ball; XmnI; BamHI; and EcoRI. Used to facilitate cassette mutagenesis of selected regions. Synthesised by phosphoramidite chemistry, by dividing desired gene into 18 oligomers. (Updated on 25-MAR-2003 to correct PA field.)
                        254 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG
 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr
                                                                          55 ValGluValileSerGluMetPheAspLeuGluGluProThrCysLeuGlnThrArgLeu
                                                                                                                                                75 GlubeuTyriysGlnGlybeuArgGlySerbeuThriysbeuLysGlyProbeuThrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic DNA; human granulocyte colony stimulating factor; restriction sites; cassette mutagenesis; expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic human granulocyte colony stimulating factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 14 and fig 3a; 21pp; English.
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P-PSDB; AAP90115.
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01-NOV-1989
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251 ATGGCTAGCCATTACAAACAGCATTGTCCGCCGACTCCGGAAACTTCTTGTGCTACTCAG 310
                                    IlelleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
                                                                        Arcarcactricgaarcrircaaagaaaaccrgaaagarrirccrgcrggrrarcccgrrc 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA including recognition site for BspMI enzyme - allowing generation of blunt end for fusion in prodn. of fusion proteins.
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                                                                                                                                                                                                                                                                                                                                                Synthetic gene for human granulocyte colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                  DNA; BspMI; restriction sites; blunt ends; fusion proteins; synthetic gene; human granulocyte colony stimulating factor.
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                                                                                                                                                                                                                    AAN90383 standard; DNA; 415
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P-PSDB; AAP90118.
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                                                                                                                                                                                                                                                               254 Argaccadecacracaagcagcacracccracaggaaacrrecrargcaaccag 313
                                                                                                                                                                                                                                                                                                                                                                                                                   1-3; CSF; colony stimulating factor; cytokine; lymphokine;
fusion protein; linker; 88.
                                                                                                                                                               55 ValGluValileSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
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                                                                                                         14 ATGGCACCCGCCCGGTCACCCCAGCCCCAGCACCCTGGGAGCATGTGAATGCCATC
                                                                                                                                                                                                GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet
                                                                                                                               35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr
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104 G; 77 T; 0 U; 0 Other;
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Thomas JW;
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Olins PO, Paik
                                                                                US-10-723-083-2 (1-142) x AAN90274 (1-415)
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                       1.67e-67
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BP; 104 A; 130
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Mckearn JP,
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P-PSDB; AAR79320.
                                                                                                                                                                                                                                                                                                                                                                                                                   hIL-3;
                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                          mutant; mutein;
               Alignment Scores:
Pred. No.:
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Sequence 415
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BK,
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RI-RE, RE-RI, RI-LE, TO TRI-RI, where RI is a mutant or variant of human interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF) including cytokine, 1ymphokine, interleukin, hematopoietic growth factor or IL-3 variant, and L is a linker. Generic sequences are described in AAW03235 - AAW03242, and specifically claimed examples are shown in comparing the present sequences are shown in AAR79342-FR9345. The fusion protein is made by recombinant DNA techniques. Specifically claimed examples of DNA sequences (including the present sequence) which encode these proteins care shown in AAQ97167-097204 and AAQ97222-097237. The fusion protein is used to increase haematopoietic cell production. It is also useful as an IL-3 antagonist or as a discrete antigenic fragment for production of antibodies useful in immunoassays and immunotherapy. Antagonists are used to block the growth of certain cancer cells and in treatment of sathma.

CThe fusion protein can also be used to stimulate bone marrow and blood cell activation and growth in vitro before infusion; and to treat diseases characterised by decreased levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic system. The protein has the usual activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects
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interleukin-3, a variant or a colony stimulating factor - useful increase haematopoietic cell prodn. in a mammal.
                                                                                                                                           fusion protein is disclosed which has the formula R1-L-R2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 822 BP; 222 A; 244 C; 180 G; 176 T; 0 U; 0 Other;
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Matches:
Conservative:
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                                                                                 Page 167-168; 447pp; English.
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1 (bases 1 to 777)

Bauer, S. Christopher., Abrams, M.Allen., Braford-Goldberg, S.Ruth., Caparon, M.Helena., Esston, A.Michaell., Klein, B.Kure., McKearn, J.P., Caparon, M.Helena., K. and Thomas, J.W.

Methods of using multivariant IL-3 hematopoiesis fusion protein Patent: US 6361977-A 55 26-MAR-2002;

Location/Qualifiers
                          AR2022 Sequence
AR20222 Sequence
AR20222 Sequence
AR20222 Sequence
AR20223 Sequence
BR20233 Hereromin
AR00335 Sequence
BR20336 Sequence
BR20336 Sequence
AR20033 Pst.-Hind I
E11628 MGM-CSF-enc
A20082 Pst.-Hind I
E11628 MGM-CSF-enc
A20083 Pst.-Hind I
I A11762 Artificial
A11763 Artificial
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CQ03172 Sequence
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I0691 Sequence
I0693 Sequence
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I0699 Sequence
A2008 Bamfi-HindI
A2008 Bamfi-HindI
A2008 Bamfi-HindI
AR223282 Sequence
A00367 Artificial
A00368 Artificial
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/wol_type="unassigned DNA"
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HUMCSFGMB
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A14305
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AR202220
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CQ721607
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DEFINITION
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JOURNAL
FEATURES
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VERSION
KEYWORDS
SOURCE
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AUTHORS
 ORIGIN
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-MODBL=frame+ p2n.model.-DEV=xlh
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AR223208 Sequence
E11629 hGM-CSF-enc
AR202280 Sequence
                                                                  ; Search time 3628 Seconds
(without alignments)
1896.538 Million cell updates/sec
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1 MHHHHHHSGIBGRMAPARS......BNLKDFLLVIPFDCWEPVQE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                              4708233 segs, 24227607955 residues
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Listing first 45 summaries
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AR223208
E11629
AR202280
                                                                   March 11, 2005, 17:26:51
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Xgapop 10.0, Xgapext (
Ygapop 10.0, Ygapext (
Fgapop 6.0, Fgapext (
Delop 6.0, Delext
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E11629 384 bp DNA linear PAT 29-SEP-1997
hGM-CSF-encoding DNA for efficient expression in E.coli.
E11629
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Matsuki,S., Ozawa,T. and Tamai,Y.
PRODUCTION OF STIMULATING FACTOR FOR HUMAN GRANULOCYTIC MACROPHAGE
                                            555
                                                                                                                           615
                                                                                                                                                                  89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
                                                                                                                                                                                                              675
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JP 1996173185-A/2
09-JUL-1996
09-JUL-1987
28-APR-1987 JP 1995263370
MATSUKI SHIGERU, OZAWA TADASHI, TAMAI YUKIO
C12P21/02,C12N1/21,C12N15/09,(C12P21/02,C12R1:19),(C12N1/21,
strandedness: Double;
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                                                                               496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT
                                                                                                                                                                                             676 ACTICCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC
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                                                                                                                                                                                                                                                                                                                                        129 LeuLeuVallleProPheAspCysTrpGluProValGlnGlu 142
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AMGEN, KIRIN BREWERY CO LTD
OS None
Artificial sequences.
PN JP 1996173185-A/2
PD 09-JUL-1996
PI MATSUKI SHIGERU, OZAWA TADASHI, TAMA PC C12P21/02, C12N1/21, C12N15/09, (C12P21/C2, C12N1/21, C12N15/09, (C12P21/C2, C12N1/21, C12N15/09, (C12P21/C2, C12N1/21, C12N15/C2, C12N1119);
CC C12R1119);
CC C12R1119;

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JP 1996173185-A/2.
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1 (bases 1 to 777)

Bauer, S.C., Abrams, M.A., Braford-Goldberg, S.R., Caparon, M.H.,
Easton, A.M., Klein, B.K., McKearn, J.P., Olins, P.O., Paik, K. and
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Methods of ex-vivo expansion of hematopoietic cells using multivariant IL-3 hematopoiesis chimera proteins
Patent: US 6436387-A 55 20-AUG-2002;
Location/Qualifiers
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Sequence 55 from patent US 6436387.
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/organism="unknown"
/wol_type="genomic DNA"
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Qy 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134 Db 301 ATTATCACCTTTGAAAGTTTCAAAGAAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360 Qy 135 AspCysTrpGluProValGlnGlu 142 Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384 RESULT 5	AR223282 LOCUS AR223282 AR223282 AR223282 AR223282 DEFINITION SEQUENCE 176 from patent US 6436387. ACCESSION AR223282 VERSION AR223282.1 GI:23331290 KEYWORS SOURCE ONGANISM Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 402) AUTHORS Bauer, S. C., Abrams, M. A., Braford-Goldberg, S. R., Caparon, M. H.,	TITLE Methods of ex-vivo expansion of hematopoietic cells using multivariant IL-3 hematopoietic cells using multivariant IL-3 hematopoietis chimera proteins unitivariant IL-3 hematopoietis chimera proteins to 6436397-A 176 20-AUG-2002; FRATURES Location/Qualifiers 1. 402 . 402	6: 1.126-59 678.00 1ty: 100.00% larity: 100.00% 6	US-10-723-083-2 (1-142) x AR223282 (1-402) Oy 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34	Db 1 ATGGCACCGGTTCTTCCCCGTCTAGCCAGCGTGGGAACGTGATGCCATC 60	75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 	Qy 95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114	Oy 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPhe 134	RESULT 6 A00367 LOCUS A00367 415 bp DNA linear PAT 09-MAR-1993
Db 61 CAGGAAGCTCGTCGTCTGTCTCGTGATACTGCTGAAATGAACGAAACT 120 Qy 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74 Db 121 GTTGAAGTGATCAGCGAAATGTTCGATCTGCAGGAACCGACTTGTCTGCAAACCGTCTG 180 Qy 75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94 Db 181 GAACTGTACAAACAGTCTGCGTGGTTCTCTGACTAAACTGAAAGGTCCGCTGACTATG 240	Qy 95 MetalaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysalaThrGln 114 Db 241 ATGGCTAGCCATTACAACAACAACACTCCGGAACTTCTTGTGCTACTCTGG AD 115 Ile11eThrPheGluSerPheLysAspPheLeuLeuValleProPhe Db 301 ATCATCACTTTCGAATCTTTCAAGAAACCTGAAAGATTTCCTGCTGTTTTCTCTGTTC AD 1135 ASPCYSTTGTUPProValGInGlu 142 Db 361 GATTGTTGGAACTCTGGGAA 384	RESULT 4	REFERENCE 1 (bases 1 to 402) AUTHORS Bauer, S. Christopher., Abrams, M.Allen., Braford-Goldberg, S.Ruth., Caparon, Helena, Easton, A.Michael., Klein, B. Kure., McKearn, J.P., Olins, P.O., Paik, K. and Thomas, J.W. TITLE Methods of using multivariant IL-3 hematopoiesis fusion protein JOURNAL Patent: US 6361977-A 176 26-MAR-2002; FBATURES Location/Qualifiers Source	/organism="unknown" /mol_type="unassigned DNA" ORIGIN	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Score: Score: Alignment Similarity: Alignment Similarity: Alignment Similarity: Alignment Similarity: Alignment Similarity: Alignment Similarity: Best Local Similarity: Best Conservative: Best Alignment Alignment Similarity: Best Local Similari	15 MetAlaProAlaArgSerProSe 	Oy 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54 	Oy 55 ValGluValI1eSerGluMetDheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 95 MetalaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114

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TFESFKENLKDFLLVIPFDCWEPVQE"
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                                             granulocyte-macrophage colony stimulating factor; synthetic gene.
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Artificial gene for granulocyte/macrophage colony stimulating
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14. .400
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Patent: GB 2212159-A 2 19-JUL-1989;
Location/Qualifiers
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DEFINITION

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Patent: GB 2212159-A 3 19-JUL-1989;
Location/Qualifiers
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GM-CSF gene (from Homo sapiens)
A14305
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Patent: GB 2212160-A
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PAT 20-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
Unclassified.
I (bases 1 to 822)

Bauer, S.Christopher., Abrams, M.Allen., Braford-Goldberg, S.Ruth., Caparon, M.Helena., Easton, A.Michael., Klein, B.Kure., McKearn, J.P.Olins, P.O., Paik, K. and Thomas, J.W.
Methods of using multivariant IL-3 hematopoiesis fusion protein Patent: US 6361977-A 69 26-MAR-2002;
Location/Qualifiers
                                                                                                                                        54
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                                                                                                                                        162 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG
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Sequence 69 from patent US 6361977.
AR202220 di:20256759
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other sequences; artificial sequences
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Patent: GB 2212160-A 3 19-JUL-1989;
Location/Qualifiers
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GM-CSF gene (from Homo sapiens).
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/gene="human GM-CSF !
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Qy 95 MetalaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114 bb 679 ATGGCCAGCACTACAAGCAGCACTGCCCTCCAACCCCGGAACTTCCTGTGCAACCCAG 738 Qy 115 IlelleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPhe 134 Db 739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798 Qy 135 AspCysTrpGluProValGlnGlu 142 Db 799 GACTGCTGGGAGCCAGTCCAGGAG 822	o Eanais ch	ignment Scor ed. No.: ore: ore: coent Simila st Local Sim ery Match: :	Db 520 AIGGCACCGGCTCCTCCCGTCTCCCGTCTCCCGTCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Qy 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54 Db 499 CAGGAGGCCCGGCGTCCTGAACCTGAGGACATGCTGCTGCTGATGAAACA 558 Qy 55 ValGluValIleSerGluMetPheAspLeuGlnGluBroThrCysLeuGlnThrArgLeu 74 Db 559 GTAGAAGTGATATCAGAAATGTTTGACTCCAGGAGCCGACTTGCCTACAGACCCGCCG 618 Qy 75 GluLeuTyrLysGlnGlyLeuArgACGTSCCCGCGCG 618 Qy 75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrILysGlyProLeuThrMet 94 Ph	Qy 95 MethlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114 Db 679 ATGGCCAGCCACTACAAGCAGCACTGCCCCGGAAACTTCCTGTGCAACCCGG 738 Qy 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPhe 134 Db 739 ATTATCACCTTTGAAAGTTTCAAAGGAACTTCCTGCTTGTCATCCCTTT 798 Qy 135 AspCysTrpGluProValGlnGlu 142 Db 799 GACTGCTGGGAGCCAGTCCAGGAG 822 RESULT 11 AR223222 LOCUS 822 bp DNA DeFINITION Sequence 69 from patent US 6436387. VERSION AR223222.1 GENENORD GIRCORD VERSION AR223222.1 VERSION AR223222.1 VERSION AR223222.1 VERSION AR223222.1 ORGANISM Unknown.	Unclassified. Unclassified. Unclassified. AUTHORS Bauer, S.C., Abrams, M.A., Braford-Goldberg, S.R., Caparon, M.H., Easton, A.M., Klein, B.K., McKearn, J.P., Olins, P.O., Paik, K. and Thomas, J.W., TITLE Methods of ex-vivo expansion of hematopoietic cells using multivariant IL-3 hematopoiesis chimera proteins JOURNAL Patent: US 6436387-A 69 20-AUG-2002; FEATURES 1822 Location/Qualifiers 1822 /organism="unknown" /mol_type="genomic DNA"	7 Mor Non 72 Mor On

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C12N15/09, A61K35/76, A61K38/00, A61K38/21, A61P35/00, A61P35/02,
C12N15/09, A61K35/76, A61K38/00, A61K38/10, C12N15/10, C12P211/02, C12N21/02, C12N21/02, C12N21/02, C12N21/02, A61K37/66,
(C12N20, C12R1:91)
Heterominibodies
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    Ľ.
    Zettl,
                                                       Homo sapiens (human)
Mus musculus (mouse)
2005251053-A/32
16-JUL-2002
28-JUL-1999 EP 2000562401
28-JUL-1998 EP 98114082.5
PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN
  Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and
Heterominibodies
Patent: JP 2002521053-A 32 16-JUL-2002;
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Matches:
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Sequence 36 from Patent W00006605.
AX023365
AX023365.1 GI:10183777

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AX023365
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1630)
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                                                                                                                                       1 (bases 1 to 903)
Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P.O., Paik,K. and
                                                                                                                                                                                  Thomas,J.W.

Methods of ex-vivo expansion of hematopoietic cells using multivariant IL-3 hematopoiesis chimera proteins
Patent: US 6436387-A 66 20-AUG-2002;
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Sequence 66 from patent US 6436387.
AR232219 GI:23331227
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JP 2002521053-A/32.
Homo sapiens (human)
Homo sapiens
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*Mufer, P., Zettl, F., Dreier, T., Baeuerle, P.A. and Borschert, K. Heterominibodies
Patent: WO 0006605-A 36 10-FEB-2000;
KUFER FPIER (DE); ZETTL FLORIAN (DE); DREIER TORSTEN (DE);
BABUERLE PATRICK (DE); BORSCHERT KATRIN (DE); MICROMET GES FUER BIOMEDIZINIS (DE)
Location/Qualifiers
1. 1630
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39-1610
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TLYLQMNSELRAEDTAVYYCAKDMGWGSGWRPYYYGMDVWGGGTTVYNSGTPLIGDTT
TLYLQMNSELRAEDTAVYSCAKDMGWGSGWRPYYYGMDVWGGGTTVTVSSGTPLGDTT
TLASSYGLYSLSSYVTVPSSSLGTQYTALGCIVVTVPPRETYVSWNSGALTSGWTFPDAV
LQSSGLYSLSSYVTVPSSSLGTQYTALGCIVVTVPPSTRTVDKKVPPKSCDKTSGGGGSAP
ARRESPSPTQPWEHVNAI QBARRILANLSKDTAAEMNETVBVISEMFDLQEPTCLQTRLE
LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITPESFKENLKDFLLVIP
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ATYFCQQSDSLPITFGQGTRLDIQGGGGSGGGGSEVQLLESGGGVVQPGRSLR
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                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Search completed: March 11, 2005, 19:37:25

Job time : 3634 secs

Perfect score:

Sequence:

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Run on:

Scoring table:

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Sequence 9, Appli
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Sequence 1, Appli
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Sequence 6, Appl
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Sequence 31, Appli
Sequence 31, Appli
                                                                                                                                                               Patent No. 5391485
Patent No. 5391485
Patent No. 529496
Patent No. 5209496
Patent No. 5200327
Saguence 7, Appli
Sequence 7, Appli
Patent No. 5200327
              Sequence
                            Sequence
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,318
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 55, Appl
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Sequence 176, App
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Sequence 176, App
Sequence 69, Appl
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                                                                                    March 11, 2005, 18:21:21; Search time 163 Seconds (without alignments) 1425.468 Million cell updates/sec
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/cgn2 6/ptodata/1/ina/6A COMB.seq:*
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/cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                             nucleic search, using frame_plus_p2n model
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US-08-46-872A-55
US-08-762-227A-55
US-08-469-118-76
US-08-468-609A-176
US-08-762-227A-176
US-08-762-227A-176
US-08-762-227A-176
US-08-762-227A-176
US-08-468-609A-69
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APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Bareford-Goldberg, Sarah R.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: McKearn, John P.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
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                 TELEPHONE: (314)77-696
TELEPAX: (314)73-6972
INFORMATION FOR SEQ ID NO: 55.
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPR: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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US-08-446-872A-55
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APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
WINDER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
                                                                                                     615
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                                                                                                                                                            29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla
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                                                                                                                                                                                                                                                                                     496 GCTGAGATGAATGAAACAGTAAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT
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3: Corporate Patent Dept.
P. O. Box 5110
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
                                     US-10-723-083-2 (1-142) x US-08-469-318-55 (1-777)
Gaps:
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Braford-Goldberg, Sarah R.
Caparon, Maire H.
Eatton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Abrams, I
APPLICANT: Bauer,
APPLICANT: Easton,
APPLICANT: Easton,
APPLICANT: MCKearn,
APPLICANT: Oling, PAPPLICANT: Paik, Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
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STREET: P.
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US-08-468-609A-55
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GENERAL INFORMATION:
APPLICANT: Abra
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                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,872A

FILING DATE: 06-JUN-1995

CLASSIPICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

ATYORNEY AGENT INFORMATION:

NAME: Bennett, Dennig A.

REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 55:

SEQUIBNCE CHARACTER STICS:

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Mismatches:
Indels:
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Matches:
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; Sequence 55, Application US/08762227A
; Patent No. 6436387
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MOLECULE TYPE: DNA (genomic)
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97.01%
97.01%
89.15%
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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Pred. No.:
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WEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIT APPLICATION DATE:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFFCATION: GUNCOWN>
PRIOR APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                              Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFRENCE/DOCKET NUMBER: C-2790/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
               Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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US-08-762-227A-55
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TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
Abrams, Mark A.
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Query Match:
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Pred. No.:
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LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
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                                                                                   LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
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196 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555
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                                                                                                     616 AAGGGCCCCTTGACCATGATGGCCACTACAAGCAGCACTGCCCTCCAACCCGGAA
                           CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu
                                                     556 receracadaccecerecadereracaaccadececerecegeceagecre
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                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Procein NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 02-FEB-1995
                                                                                                                                                                                             LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                             Sequence 55, Application PC/TUS9501185
GENERAL INFORMATION:
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Pred. No.:
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Best Local Similarity:
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109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
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616 AAGGGCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCGGAA
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US-08-469-318-176

Sequence 176, Application US/08469318

Patent No. 6022535

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Protein

NUMBER OF SEQUENCES: 196

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,318

FILING DATE:

INFORMATION POR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

INFORMATION TOR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

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SEQUENCE CHARACTERISTICS:

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95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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                                                                                                                                                                           55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu
                                                                                                                                                                                                                                                                                                     75 GlubeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet
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APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Caparon, Maire H.
APPLICANT: Caparon, Maire H.
APPLICANT: Klein, Barbara K.
APPLICANT: Klein, Barbara K.
APPLICANT: Olins, Peter O.
APPLICANT: Olins, Peter O.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Pusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN 1995
CLASSIFICATION 7424
PRIOR APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTONNEY/AGENT INPORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co. ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: 1111nois
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Patent No. 6361977
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: C-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 737-6986
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APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
APPLICANT: Thomas, John W.
APPLICANT: Thomas, John W.
APPLICANT: Paik, Kumnan
APPLICANT: Paik, Kumnan
APPLICANT: Paik, Kumnan
APPLICANT: Paik, Kumnan
APPLICANT: Secous John W.
APPLICANT: Secous John W.
APPLICANT: Secous John W.
APPLICANT: John
                                           301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCTTT 360
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Ocroporate Patent Dept.
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
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Mismatches:
Indels:
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Matches:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEFORM: (314)737-6986
TELEFAX: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
                                                                                                           135 AspCysTrpGluProValGlnGlu 142
                                                                                                                                                                        361 cacrecreceacceaerceaeae 384
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US-08-468-609A-176
Sequence 176, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: nucleic acid
STRANDEDNESS: double
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Query Match:
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MOLECULE TYPE:
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Percent Similarity:
Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSE: Dennis A. Bennett, G.D. Searle & Co.
Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: 111inois
COMMITX: USA
ZIP: 60680
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TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
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Mismatches:
Indels:
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                                                                                                    Length:
Matches:
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Bauer, S. C.
Barford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-08-762-227A-176
; Sequence 176, Application US/08762227A
; Patent No. 6436387
; GENERAL INFORMATION:
 TYPE: nucleic acid
STRANDENDESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                   2.23e-76
678.00
100.00%
100.00%
nucleic acid
                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                ; MOLECULE TYPE
US-08-446-872A-176
                                                                                       Alignment Scores:
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DB:
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241 ATGGCCAGCCACTACAAGCAGCAGCACTGCCCTCCAAACCTCCTGTGCAAACCAG
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Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
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                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION OATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/46,872
FILING DATE: 06-JUN 1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 176:
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PCT-US95-01185-176
; Sequence 176, Application PC/TUS9501185
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Protein
; TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 402 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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Patent No. 6030812
GENERAL INFORMATION:
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Best Local Similarity:
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US-08-468-609A-69
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Pred. No.:
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Sequence 69, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
FILLING DATE: 02-FEB-1995
                                                                                                                                                                                                                                                                                                                                     402
128
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Mismatches:
Indels:
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Matches:
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                                                                                                               FILING DATE: 02-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-08-469-318-69
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APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Braton, Maire H.
APPLICANT: Caston, Maire H.
APPLICANT: McKeart, John P.
APPLICANT: Thomas, John W.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGAATGCCATC 498
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PatentIn Release #1.0, Version #1.30 (EPO)
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Matches:
Conservative:
Mismatches:
Indels:
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                                     US/08/469,318
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                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
                                                                                                                                FILING DATE:
INFORMATION FOR SEG ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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678.00
100.00%
100.00%
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                  CURRENT APPLICATION DA APPLICATION NUMBER:
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Query Match:
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                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-UNN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTONNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REGISTRATION NUMBER: 34,547
REGISTRATION NUMBER: 34,547
REGISTRATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFEKK: (314)737-6986
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Matches:
Conservative:
Mismatches:
Indels:
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ADDRESSEE: Dennis A. Bennett, G.D. ADDRESSEE: Corporate Patent Dept. STREET: P. O. Box 5110 CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60680
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678.00
100.00%
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88.63%
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nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
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1128
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TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      E: Dennis A. Bennett, G.D. Searle & Co.
E: Corporate Patent Dept.
P. O. Box 5110
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REPERENCE/DOCKET NUMBER: C-2790/1
TELECOMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 1180RATION:
TELECHMUNICATION 1180RATION:
TELECHMUNICATION 1180RATION:
                                                                                     Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Sequence 69, Application US/08446872A Patent No. 6361977
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MOLECULE TYPE: DNA (genomic)
                                                                     Abrams, Mark A.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dennis
ADDRESSEE: Corpor
STREET: P. O. Box
CITY: Chicago
STATE: 111inois
COUNTRY: USA
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Best Local Similarity:
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95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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                                                                                                                                                                                                                                                     15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 02-FEB-1995
CLASSIFICATION:
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
   SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-08-762-227A-69
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GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 69:
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LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                     Percent Similarity:
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Pred. No.:
Score:
                                                             Alignment Scores:
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                                                                                 Pred. No.:
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619 GAGCTGTACAAGCAGGGCCTGCGGGCAGCTCACCAAGCTCAAGGGCCCCTTGACCATG 678
                                                                                                                                     MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
                                                                                                                                                                         679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCAG 738
                                                                                                                                                                                                             115 IlelleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPhe 134
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COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., Corporate Patent Dept.
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abrams, Mark A.
Bauer, S. C.
Bradford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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REGISTRATION NUMBER: 34,547
REFRENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
                                                                                                                                                                                                                                                                                           135 AspCysTrpGluProValGlnGlu 142
                                                                                                                                                                                                                                                                                                             799 GACTGCTGGGAGCCAGTCCAGGAG 822
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 69, Application US/08762227A Patent No. 6436387 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: Illinois
COUNTRY: USA
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ю	35 GlnGluAla	ArgArgLeuLeuAsn	LeuSerArgAspThr	GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr	54
499		CGGCGTCTCCTGAAC	CTGAGTAGAGACACT	CAGGAGGCCCGGCGTCTCCTCGAACCTGAGTAGAGACACTGCTGCTGCTGAGATGAATGA	558
Ľ	S	IleSerGluMetPhe	AspleuGlnGluPro	ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu	74
559		ATATCAGAAATGTTT	GACCTCCAGGAGCCG	GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG	618
7	75 GluLeuTyr	LysGlnGlyLeuArg	GlySerLeuThrLys	GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet	94
619		AAGCAGGCCTGCGG	GGCAGCCTCACCAAG	GAGCTGTACAAGCGCCCTGCGGGCCAGCCTCACCAAGCTCAAGGGCCCCCTTGACGA	678
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115		PheGluSerPheLys	lleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVal	PheLeuLeuValileProPhe	134
739		TTTGAAAGTTTCAAA	GAGAACCTGAAGGAC	ATTATCACCITTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT	798
135	AspCy	sTrpGluProValGlnGlu	142		
799		GACTGCTGGGAGCCAGTCCAGGAG	822		

Search completed: March 11, 2005, 20:27:22 Job time : 167 secs

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Sequence 31, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 16, Appl
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Sequence 2, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 30, Appli
Sequence 30, Appli
                                                                                                        Sequence 55, Appl
Sequence 176, App
Sequence 69, Appl
Sequence 66, Appl
Sequence 9, Appli
Sequence 141, App
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Sequence 19, Appl
Sequence 21, Appl
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Seguence 165, App
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Sequence 33, Appl
Sequence 34, Appl
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Sequence 31,
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                                                                         Sequence
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; Publication No. US20050050602A1
; GENERAL INFORMATION:
    APPLICANT: Altosaar, Illimar
; APPLICANT: Bardana, Ravinder
; APPLICANT: Dudani, Aail
; APPLICANT: Tackaberry, Billeen
; TITLE OF INVENTION: Production of GM-CSF in Plants
; FILE REFERENCE: O8-898901US
; CURRENT APPLICATION NUMBER: US/10/723,083
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: Canada 2,410,702
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 3
                                                                   US-10-723-083-3

US-10-723-083-1

US-10-083-446-176

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US-10-083-446-96

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                                                                                                                              March 11, 2005, 19:37:32 ; Search time 505 Seconds (without alignments) 1672.655 Million cell updates/sec
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                 GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                            nucleic search, using frame_plus_p2n model
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Scoring table:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 TTCAAAGAGAACCTGAAGGACTTCCTGCTTGTGTTCATCCCCTTTGACTGCTGGGAGCCAGTC 420
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Conservative:
Mismatches:
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Fublication No. US20050050602A1
GENERAL INFORMATION:
APPLICANT: Altosaar, Illimar
APPLICANT: Sardana, Ravinder
APPLICANT: Ganz, Peter
APPLICANT: Tackaberry, Eilleen
TILLE OF INVENTION: Production of GM-CSF in Place
FILLE REFERENCE: 08-98991US
CURRENT APPLICATION NUMBER: US/10/723,083
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: Canada 2,410,702
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SOFTWARE: Patentin version 3.1
SEQ ID NO L
LENGTH: 458
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
; OTHER INFORMATION:
US-10-723-083-3
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ORGANISM: Homo sapiens
FEATURE:
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US-10-723-083-1
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Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
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ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation Corporate Pacent Dept., Mail Zone 04E
                                                                                                     458
142
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Matches:
Conservative:
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Indels:
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US-10-083-446-55
i Sequence 55, Application US/10083446
i Publication US/2030185790A1
i GENERAL INFORMATION:
i APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sar
i Raford-Goldberg, Sar
i Raford-Maire H.
Raston, Alam M.
Klein, Barbara K.
Klein, Barbara K.
NCKearn, John P.
Olins, Peter O.
Paik, Kumnan
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
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; OTHER INFORMATION:
US-10-723-083-1
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Best Local Similarity:
Query Match:
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Pred. No.:
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Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <unimal color with the color with t
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REGISTRATION INDRER: -2.305
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
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ULE TYPE: DNA (genomic)
SNCE DESCRIPTION: SEQ ID NO: 176:
                                                                                                                                               æ
                                                                                                                                               Sarah
equence 176, Application US/10083446 iblication No. USZ00030185790A1 GENERAL INFORMATION: APPLICANT: Abrams, Mark A.
                                                                                              Abrame, S. C.
Bauer, S. C.
Braford-Goldberg, &
                                                                                                                                                                           Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
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INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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STATE: Missouri
COUNTRY: USA
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Best Local Similarity:
Query Match:
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Pred. No.:
   Sequence 176,
Publication N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 GluhisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla
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                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
RILING DATE: 06-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-723-083-2 (1-142) x US-10-083-446-55 (1-777)
                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446
FILING DATE: 26 Feb-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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Best Local Similarity:
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US-10-083-446-176
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TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
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                                                                                                                                                                                                                                                                                                                                                   15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle
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ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
                                                                                                                                                                           822
128
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-083-446-66
i Sequence 66, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S.
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Braford-Goldberg, S. Caparon, Maire H.
Easton, Alam M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
                                                           TOPOLOGY: linear
ULE TYPE: DNA (genomic)
ENCE DESCRIPTION: SEQ ID
       LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                           2.98e-80
678.00
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100.00%
88.63%
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STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
                                                                               MOLECULE SEQUENCE SEQUENCE US-10-083-446-69
                                                                                                                                                           Alignment Scores:
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Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
                                                                                                                                       MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                 74
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                                   ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu
                                                                                                           GluLeuTyrLygGlnGlyLeuArgGlySerLeuThrLygLeuLygGlyProLeuThrMet
                                                                         121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Pb-2002
CLASSIFICATION NUMBER: 08/762,227
APPLICATION NUMBER: 08/762,227
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-PBB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY AGENT INCORMATION:
NAMELY AGENT INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             135 AspCysTrpGluProValGlnGlu 142
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Braford-Goldberg, S.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 69, Application US/10083446
Sequence 69, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILEPHONE: (636)737-6257
ILEFAX: (636)737-5452
FOR SEQ ID NO: 69:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                    PRICATION DAMBER: US/10/083,446
FILING DATE: 26-Peb-2002
CLASSIFICATION: CURROWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DE-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-PEB-1994
APPLICATION NUMBER: US 08/446,872
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-723-083-2 (1-142) x US-10-083-446-66 (1-903)
                                                                                                                                                                                                                                                                                                 NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
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                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
TELEPHONE: (636)737-6257
TELEPAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 66
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 903 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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678.00
100.00%
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88.63%
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Best Local Similarity:
Query Match:
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Pred. No.:
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; Sequence 9, Application US/10609346

10-609-346-9

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Publication No. US20040063635A1
GENERAL INFORMATION:
APPLICANT: Yu, Zailin
APPLICANT: Yu, Zailin
APPLICANT: Fu, Yan
TITLE OF INVENTION: REFECTS
FITLE OF INVENTION: REFECTS
FILE REFERENCE: ZVU-0603
CURRENT FILING DATE: 2003-06-26
PRIOR FILING DATE: 2003-06-26
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 2211
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Sequence 141, Application US/10449831A

Publication No. US20040029179A1

GENERAL INFORMATION:

APPLICANT: Koentgen, Frank

TITIE OF INVENTION: Higher molecular weight entities and uses therefor TITIE REFRENCE: 2385978

CURRENT APPLICATION NUMBER: US/10/449,831A

CURRENT FILING DATE: 2003-05-30

PRIOR FILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 237

SOFTWARE: Patentin version 3.2
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127
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: DNA of HSA-GMCSF
US-10-609-346-9
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.98e-79
675.00
100.00$
99.22$
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Best Local Similarity:
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US-09-826-025-8
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                                                                                                                                                                                                                                                                                                                                                                                     AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                               IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPheAsp 135
                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
                                                                                                                                                                                                                                                      GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
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                                                                                                                                                                                                                                                                                               GluValileSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                          GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                            429
0 0 0
0 0 0
                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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PPLICATION NUMBER: US/09/826,025
FILING DATE: 04-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA: APPLICATION NUMBER: 08/838,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 TGCTGGGAGCCAGTCCAGGAG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                          5.58e-80
673.00
100.00%
100.00%
87.97%
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                                                                                                                                Percent Similarity:
Best Local Similarity:
                                        FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...

US-10-449-831A-141
                     TYPE: DNA
ORGANISM: Human
                                                                                                Alignment Scores:
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US-09-826-025-8
SEQ ID NO 141
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                                                                                                          No.:
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GCACCCGCCCCCCCAGCCCCAGCACCCCTGGGAGCATGTGAATGCCATCCAG 111
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APPLICANT: IATROU, KOSEAS
APPLICANT: IATROU, KOSEAS
APPLICANT: BEHIEL, PALTICK J.
APPLICANT: BEHIEL, LEO A.
ITILE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF
ITILE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
FILE REFRENCE: 0.29722-20.
CURRENT APPLICATION NUMBER: US/10/083,590
CURRENT PILING DATE: EARLIER APPLICATION NUMBER: 09/256,694
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: EARLIER PAPPLICATION NUMBER: US 09/136,421
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                        NAME: Ingolia, Diane B.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CHI
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysTrpGluProValGlnGlu 142
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; Publication No. US20030027257A1
; GENERAL INFORMATION:
                                                                                                                                                                  TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            LENGTH: 435 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
FILING DATE: <Unknown.
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US-10-083-590-14
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352 ATCACCTTCGAGGACTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGAC 411
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| Publication No. US2004000934A1
| GENERAL INFORMATION:
| APPLICANT: Lai, Wan-Ching
| APPLICANT: Clu, Yong Liang
| APPLICANT: Chu, Yong Liang
| APPLICANT: Chu, Yong Liang
| APPLICANT: Trank Q.
| TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
| FILE REFERENCE: 3781-004-27
| CURRENT APPLICATION NUMBER: US/10/188,056
| CURRENT FILING DATE: 2002-09-26
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 32
| LENGTH: 435
| TYPE: DNA
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US-10-188-056-32
   Percent Similarity:
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US-10-188-056-32
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056,871
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 435
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US-10-188-056-31
Sequence 31, Application US/10188056
Publication No. US20040009934A1
GENERAL INFORMATION:
APPLICANT: Chu, Jian-Tai
APPLICANT: Lai, Wan-Ching
APPLICANT: Lai, Frank
APPLICANT: Li, Frank
TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
FILE REFERENCE: 3781-004-27
CURRENT APPLICATION NUMBER: US/10/188,056
CURRENT PILING DAFE: 2002-09-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 435
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Best Local Similarity:
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ORGANISM: Human
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US-10-411-026-17

US-10-411-026-17

US-10-411-026-17

Publication No. US20040063911A1

GRENEAAL INFORMATION:

APPLICANT: Neces Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: DeFrees, Shawn

APPLICANT: BAYER, David

APPLICANT: Hakes, David

APPLICANT: BAYER: US/10/411,026

CURRENT FILMS DATE: 2003-04-09

FILMS APPLICATION NUMBER: US 60/328,523

FRIOR APPLICATION NUMBER: US 60/329,523

FRIOR APPLICATION NUMBER: US 60/339,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR PLING DATE: 2002-06-07

PRIOR PLING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-17

PRIOR PLING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR PRIOR
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        36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal
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Sequence 17, Application US/10411037

Publication No. US20040043446A1

GENERAL INPERMITION:

APPLICANT: Neger Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: DeFrees, Shawn

APPLICANT: Bayer Kneart

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APPLICANT: APPLICANT: Bayer

APPLICANT: APPLICANT: Bayer

APPLICANT: APPLICANT: Bayer

APPLICANT: DAYER: 2003-04-05

PRIOR PAPLICATION NUMBER: US 60/391,777

PRIOR PELING DATE: 2002-06-05

PRIOR PELING DATE: 2002-06-05

PRIOR PELING DATE: 2002-06-17

PRIOR PELING DATE: 2002-06-18

PRIOR PELING DATE: 2002-08-18

PRIOR PELING DATE: 2002-0
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                                               GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCGGCCTGGAG 231
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                                                                                                             LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet
                                                                                                                                                    CTGTACAAGCAGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGCCCCCTTGACCATGATG
GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu
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ORGANISM: Homo sapiens
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US-10-411-037-17
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US-10-410-952-17
US-10-410-952-18
US-10-
                                                                             96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
                                                                                                                                                                                                                                                                                                                                                                                                            292 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 351
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Conservative:
Mismatches:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 17
LENGTH: 435
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US-10-410-962-17
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                     GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
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or74f05.8 UI-H-FT1-

714908 MA hb05e10.g

CES009198

zb77g08.g wc88f12.x

TgESTzyj5 606916 MA

Pan trogl TgESTzyj5 TgESTzyj4 Forward B

606148 MA EST363191 UI-H-FT2-

Perfect score: Sequence: Scoring table:

Searched:

Minimum I Maximum I

1

OM protein

Run on:

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Porward
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CK144209 AGENCOURT
BU865195 S050D01 P
AJ819401 AJ819401
                               CD369973 U1-H-FT1-BU633411 U1-H-FT1-BU633411 U1-H-FT1-CA307828 U1-H-FT1-CA307828 U1-H-FT1-CA307828 U1-H-FT1-CA307828 U1-H-FT1-CA30786 U1-H-FT1-CA30786 U1-H-FT2-CA30786 U1-H-FT2-CA307871 U1-H-FT2-CA307871 U1-H-FT2-CA3078 U1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW207707
UI-H-BIZ-age-e-09-0-UI.sl NCI CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2724184 3', mRNA sequence.
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2724184"
/lab_host="DH10B (Life Technologies)"
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                                                                         CA307828
AA995402
CD368851
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AF179193
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Unpublished (1997)
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AW207707
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  LOCUS
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-MODBL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFPO_spool/US10723083/runat_08032005_131716_10436/app_query.fasta_1.327
-Q=/cgn2_1/USFPO_spool/US10723083/runat_08032005_131716_10436/app_query.fasta_1.327
-Q=/cgn2_1/USFPO_spool/US10723083/runat_08090m062_1_EOOPEL=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=000-TR MIN=0 -ALIGN=15 -MODB=LOCAL
-UNFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10723083 @CGN 1 1 4352 @runat_08032005_131716_10436 -NCPU=6 -ICPU=3
-NOWANP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FCAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPOX=0.5 -DELOP=6 -DELEXT=7
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BE873976 601484045
CF341802 TGESTZYJ4
CF370966 TGESTZYJ5
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BX111836 BX111836
BE218982 hv47a07.x
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(without alignments)
1915.353 Million cell updates/sec
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                                                                                                                                                                                                             US-10-723-083-2
765
1 MHHHHHHHSSGIBGRMAPARS......BNLKDFLLVIPFDCWEPVQE 142
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BE671554
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                              nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BX111836
BE218982
                                                                                                                                      March 11, 2005, 18:16:26
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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DB seq length: 200000000
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9b_est2:

9b_htc:

9b_est4:

9b_est6:

9b_gs81:

9b_gs81:
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Database :

673 673 673 673 673 673 668

Result Š

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Homo sapiens (nument)

Homo sapiens (nument)

Homo sapiens

Hadraca; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalis; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lobaes 1 to 658)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Human Unigeneset - RZPD3

Londact: Ina Rolfs

RZPD Deutsches Ressourcentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAG98C104601.

RZPD IMAG98C104601.

RZPD IMAG98C104061.

RZPD Deutsches Ressourcentrum fuer Genomforschung GmbH

Human UnigeneSet - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/Cgi-
bin/showlib.pl.cgi/response?libNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubmerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

www.rzpd.de

This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCACACACAGGAAACAGCTATGAC.

Location/Qualifiers

1rce
                                                                                                                                                                        BX111836 CGAP LuS Homo sapiens cDNA clone IMAGp998C104061; IMAGE:1601601, mRNA sequence.
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                         BX111836.1 GI:27837278
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Best Local Similarity:
Query Match:
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AUTHORS
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          /note=Tvector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The Note=Tvector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub2 library which is a subtracted library derived from the NCI_CGAP_Edot in Bi. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_Pr23, NCI_CGAP_Edot, NCI_CCGAP_Edot, NCI_CGAP_Edot, NCI_CCGAP_Edot, NCI_CCG
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Matches:
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/clone_lib="NCI_CGAP_Sub4"
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In Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoelmage: llni.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE218982 Hord CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176532 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                         439 CTGTACAAGCGCGGGGCCTGCGGGGCCCCTCACCAAGCTCAAGGGCCCCCTTGACCATGATG 380
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                                                                                                                GluvalIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu
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/db_xref="taxon:9606"
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COMMENT

Alignment Scores:

ORIGIN

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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

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CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NIT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llni.gov/bbrp/image/finage.html
Insert Length: A. S. Std Error: 0.00
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Length:
Matches:
Conservative:
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                                                                                                                                                                                     (1-660)
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High quality sequence stop: 4
Location/Qualifiers
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Homo sapiens
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Pred. No.:
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                                       /clone libe="NCIC CGAP Lu24"
/rote="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Plasmid DNA from the normalized library NCI CGAP LuS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 141991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE671554 Innear EST 08-SEP-2000 CASSINOTA NOT CGAP LU24 Homo sapiens cDNA clone IMAGE:3286237 3' Similar to gb:Mil220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING CATCAR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             176 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 235
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NCI-CGAP 1 to 673.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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127
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Matches:
Conservative:
Mismatches:
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/clone="IMAGE:2340997"
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Unpublished (1997)
Contact: Robert Strausberg, E
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 TGCTGGGAGCCAGTCCAGGAG 436
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Bmmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.AG.E. Consortium/LLNL, send email to: infoahange. Illigov
Seq primer: -40UP from Gibco
High quality sequence stops: 440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B. (bases 1 to 895)

B. (bases 1 to 895)

NIH-MGC http://mgc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/OTP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, inc.

CDNA Library Preparation: Life Technologies, inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MG.E. Consortium/LLNL at:

http://image.lnl.gov

Plate: LLAM9663 row: j column: 12

High quality sequence stop: 711.
                                                                                                                                                                                                                                                                                             BE873976 895 bp mRNA linear EST 20-OCT-2000
601484045F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886571 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/db Xref="taxon:9606"
/clone="ImAGE:3866571"
/tissue type="large cell carcinoma, undifferentiated"
/lab_hogt="DH108 (phage-resistant)"
/clone lib="NHH MGC 69"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Reverage insert size 1.1 kb. Library constructed by Life
Technologies."
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                                                                              392 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTGTCATCCCCTTTGAC 451
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                                                                                                                                               136 CysTrpGluProValGlnGlu 142
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Homo sapiens
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BE873976
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@inage.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
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/ db xref="taxon:9606"
/ clone="INAGE:1283742"
/ tlasue type="carcinoid"
/ tlab_host="labloB"
/ clone="INAGE:1283742"
/ tlasue type="carcinoid"
/ lab_host="DH10B"
/ clone=lb="MOT_CGAP_Lu24"
/ note="Organ: lung: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NOT_CGAP_LuS was prepared, and ss circles were made in virro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                               Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 695)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Indels:
FACTOR PRECURSOR (HUMAN);, mRNA sequence.
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/organism="Homo sapiens"
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Homo sapiens
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following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--
GCCCGCTCGCCCACCGATCC3'where n=3-4 G nucleotides.
WARNING: the library contains a small percentage of CDNAs
derived from the human host cells. Library materials
provided by David Sibley, Washington University."
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1003 Dp mRNA linear EST 27-AUG-2003 TGESTZYJ58e12.yl TG CAST Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TGESTZyJ58e12.yl 5' similar to SW:CSF2_HUMAN P04141 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR FRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 GAAGTCATCTCAGAAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCCCTGGGAGCATGTGAATGCCATCCAG 143
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Sarcocystidae: Toxoplasma.

I (bases I to 52)

Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Rillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tasgareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R., Toxoplasma EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
BamHI/EcoRI sites. The modified polylinker
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Conservative:
Mismatches:
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Toxoplasma gondii
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//moi type="me
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40up from Gibco.
Location/Qualifiers
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TgESTzyj43f02.yl Tg CAST Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TgESTzyj43f02.yl 5' similar to SW:CSF2_HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR;; mRNA
                        95
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Toxoplasma gondii
Toxoplasma gondii
Toxoplasma gondii
Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.

1 (bases 1 to 584)
Tang, K., Colé, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M.,
Tang, K., Colé, R., Martin, J., Wylie, T., Dante, M., Marra, M.,
Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
Ritter, E., Bennett, J., Franklin, C., Tasgareishvili, R., Ronko, I.,
Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
                                                   290 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCAGATT
                                                                                                                                  AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle
                     LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                             /clone lib= brectioned by the Corl bibrary /clone lib= brectioned by the Corl bibrary CAST Tachyzoite cDNA Library Mas Constructed by Mores Twector: Modified pBluescript (BBS SK+); Site_1: BamHi, Site_2: BcoRi; The CDNA library was constructed by Kellang Tang, and Robert Cola at Washington University. CDNA was synthesized from poly(A)+ mRNA using the template-switching PCR method (SNART DNA Kit, BD Bloosiences). First strand CDNA was reverse transcribed using the CDS III/3' primer and a 5' template switch primer (Snart IV primer). The product of the first strand synthesis was PCR amplified using the same primer set and the fragments were digested with Sfil. The fragments were size selected, ligated into a modified pBluescript wector (obtained from Michael White, Montana State University) containing directional Sfil sites, and electroporated into ElectroTen Blue cells. Vector: Sfil sites were added to the multiple cloning region of pBluescript SK+ between the BamHi/EcoRi sites. The modified polylinker has the BamHi/EcoRi sites. The modified polylinker has the BamHi/EcoRi sites.
Email: toxx@watson.wustl.edu
Contact David Sibley (toxxest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -400P from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGGCCTGGGCCACGGATCC3'where n=3-4 G nucleotides.
WANNING: the library contains a small percentage of CDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 265
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                                                                                                                                                     /mol_type="mRNN"
/db xref="taxon:5811"
/clone="Tgge="Tayj58e12.y1"
/lab_host="Tachyzoite"
/lab_host="ElectroTen Blue cells (Stratagene)"
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Conservative:
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@nages.llnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MAGE:3706893"
/tissue type="carcinoid"
/lab.host="blub108"
/clone lib="MCI CGAP Lu24"
/note="Corgan: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylahker; Plasmid DNA from the normalized library NCI CGAP Lu24 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs library library) subtraction by Bento
                                                                                                        BF938995 565 bp mRNA linear EST 22-JAN-2001
7r05fil.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3706893 3'
similar to SW:CSF2 HUMAN P04141 GRANULCYTE-MACROPHAGE
COLONY-STIMULATING_FACTOR PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
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                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 565)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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446 TGCTGGGAGCCAGTCCAGGAG 466
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Homo sapiens
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                                                                                                                                115
                                                                                                                                                                                                                                       115 lelleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPheA 135
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TGESTZYJ55e12.Y1 TG CAST Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TGESTZyJ55e12.y1 5' similar to SW:CSF2_HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR FRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seg primer: -40UP from Gibco.
                                  392 TTATCACCTTTGAAAGTTTCAAAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang, K., Cole, R., Pogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Kalter, E., Bennett, J., Franklin, C., Tasgaraishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R., Toxoplasma BST Project
Unpublished (2001)
                                                                                                                   etAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnI
   lubeuTyrLysGlnGlybeuArgGlySerbeuThrLysbeuLysGlyProbeuThrMetM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxoplasma gondii
Bukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida;
Sarcryotsidae; Toxoplasma.
1 (bases 1 to 585)
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                                                                                                                                                                                                                                                                                                                                                                                                452 ACTGCTGGGAGCCAGTCCAGGAG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxo@watson.wustl.edu
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DEFINITION
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COMMENT
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CD369973 718 bp mRNA linear BST 05-AUG-2004 UI-H-FTI-bke-o-08-0-UI.sl NCI_CGAP_FTI Homo sapiens cDNA clone CD.H-FTI-bke-o-08-0-UI 3', mRNA sequence.
BamHI/EcoRI sites. The modified polylinker has the following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--GGCCGCTGGGCCCACGGATCC3'where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryogia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 718)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 AlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 GAGGCCGGGGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGCTGAGATGAATTTAATAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 CTGTACAAGCAGGGCCTGCGGGGCAGCCCCACCAAGCTCAAGGGCCCCTTGACCATGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlualaargargLeuLeuAsnLeuSerArgaspThralaalaGluMetAsnGluThrval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluVallleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu
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123
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Mismatches:
Indels:
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Matches:
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CD369973.1 GI:31154063
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96.85%
84.58%
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/clone="UT-H-FLL-Boul-15-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FL1"
/lab host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FL1"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: ECOR I;
Site_2: Not I; NCI CGAP_FL1 is a normalized CDNA library
derived from a pool of mRNA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand CDNA
synthesis was primed with an oilgo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an ECOR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oilgonuclecitde used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GAGGTCGGTG. The cell lines were provided by Dr. James
Martin from the University of Iowa.
TAG TISSUB-Human Chondrosarcoma Grade 3 cell line mix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-46, >AT_rich#Low_complexity 60-129,
>(TAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU633411 701 bp mRNA linear EST 23-SEP-2002
UI-H-FL1-bgu-1-15-0-UI.s1 NCI CGAP_FL1 Homo sapiens cDNA clone
UI-H-FL1-bgu-1-15-0-UI 3', mRNA sequence.
                                                                             477 AGCCACTACAAGCAGCACCACCCACAAACTTCCTGTGCAACCCAGATTATC 418
                                                                                                                                                                                                                   417 ACCTITGAAAGTITCAAAGAGAACCIGAAGGACTITCIGCTIGICAICCCCTITGACIGG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 701)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                      SerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIleIle
                                                                                                                                                                            117 ThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVallleProPheAspCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="taxon:9606"
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TAG_SEQ=GAGGTCGGTG"
                                                                                                                                                                                                                                                                                                                                                         357 TGGGAGCCAGTCCAGGAG 340
                                                                                                                                                                                                                                                                                                              137 TrpGluProValGlnGlu 142
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VERSION
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BU633411/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 TyriysglnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetAla 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValileSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeu 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGlu 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 AlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGlu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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                                                                                                                                                                     | Mol_type="mRNA" | Color | Mol_type="maxon" | Colore="UI-H-FT1-bke-0-08-0-UI" | Cissue_type="Alveolar Macrophage"
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                                                                  Location/Qualifiers
Seq primer: M13 FORWARD POLYA=Yes.
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Best Local Similarity:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
flrom Dr. M. Bento Soares, bento-soares@wiowa.erg
The following repetitive elements were found in this cDNA
sequence: 1-50, AT_rich#Low_complexity 64-133,
SGQ primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA307828 666 bp mRNA linear EST 05-AUG-2004
UI-H-FTI-bhx-f-10-0-UI.81 NCI CGAP FTI Homo sapiens cDNA clone
UI-H-FTI-bhx-f-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                LeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAlaSerHisTyrLys 100
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1 (Dases 1 to 666)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAI-CAAP dancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                 CTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAA
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              Length:
Matches:
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           2.02e-56
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80.26%
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                                          Percent Similarity:
Best Local Similarity:
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Alignment Scores:
Pred. No.:
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CA307828/c
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1. .666
/organism="Homo sapiens"
/mol_type="mRNA"

source

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/db xref="taxon:9606"
/clone="UI-H-FTI-bhx-f-10-0-UI"
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/dev stage="Alveolar Macrophage"
/dev stage="Alveolar Macrophage"
/dev stage="Alveolar Macrophage"
/dev stage="Alveolar Macrophage"
/clone_lib="MCI_CGAP_FTI"
/note="Organ: Ling; Vector: pTYT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized compliant Macrophage challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 3 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 3 hours; Rebsiella moi 10, 24 hours; Rebsiella moi 10, 3 hours; Rebsiella moi 10, 24 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 24 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 24 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 24 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus + LPS 24 hours; Adenovirus moi 500, 24 hours; Adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; Adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt ad
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TAG LIB-UI-H-FT1
TAG SEQ-GGCCATGCCG"
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Insert Lenght: 747 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 308.
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/clone_libe_NTGIC CGAP_Lus"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                          EST 27-AUG-1998
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                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 475) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Banal: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                              or74f05.81 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1601601 3 similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN);, mRNA sequence.
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Conservative:
Mismatches:
Indels:
                                                                                                                          mRNA
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/db_xref="taxon:966"
/clone="lmAgE:1601601"
/tissue_type="carcinoid"
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365 TTTGACTGCGAGCCAGTCCAGGAG 339
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AUTHORS
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95 tAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIl 115
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174 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 TATCACCTCTTGAAGTTTCAAAGAACCTGAAGGACTTTCTGCTTGTCATCCACTTTGA 412
                                                                                95
                                                                                76 LeuTyrLysGlnGlyLeuArgGlySer-LeuThrLysLeuLysGlyProLeuThrMetMe
                                                                                                                         234 CTGTACAAGCAGGCCTGCGTGGCAGTCCTCACCAAGCTCAAGGGCCCCTTGACCATGAT
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